

GenCore version 5.1.6
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protein - protein search, using sw model

on: October 27, 2004, 16:51:34 ; Search time 23.1174 Seconds
 (without alignments)
 665.548 Million cell updates/sec

file: US-10-000-439-3

refct score: 1260
 quence: 1 EPKSCDKTHTCPPCAPELL.....MHEALTHNHYQORSLSLSPGK 232

oring table: BL03UN62
 Gapop 10.0 , Gapext 0.5

arched:

total number of hits satisfying chosen parameters: 478139

minimum DB seq length: 0
 maximum DB seq length: 2000000000

rst-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

tabase :

Issued Patents AA:
 1: /cgn2_6/pctodata/1/iaa/15A COMB.pep:
 2: /cgn2_6/pctodata/1/iaa/15B COMB.pep:
 3: /cgn2_6/pctodata/1/iaa/6A COMB.pep:
 4: /cgn2_6/pctodata/1/iaa/6B COMB.pep:
 5: /cgn2_6/pctodata/1/iaa/PC7US COMB.pep:
 6: /cgn2_6/pctodata/1/iaa/backfins1.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1225	97.2	232	2	US-08-595-043A-50	Sequence 50, Appli
2	1225	97.2	232	4	US-09-988-362A-26	Sequence 26, Appli
3	1225	97.2	331	3	US-09-178-69A-2	Sequence 1, Appli
4	1225	97.2	331	4	US-09-761-413-2	Sequence 2, Appli
5	1225	97.2	360	3	US-09-180-100-11	Sequence 11, Appli
6	1225	97.2	371	1	US-08-236-111-7	Sequence 7, Appli
7	1225	97.2	371	3	US-08-457-918-7	Sequence 7, Appli
8	1225	97.2	371	4	US-10-157-408-7	Sequence 7, Appli
9	1225	97.2	376	3	US-08-180-100-2	Sequence 22, Appli
10	1225	97.2	396	2	US-08-784-512-3	Sequence 3, Appli
11	1225	97.2	396	3	US-09-176-228-3	Sequence 3, Appli
12	1225	97.2	424	5	PCT-US95-03866-12	Sequence 12, Appli
13	1225	97.2	424	5	PCT-US95-03866-14	Sequence 14, Appli
14	1225	97.2	437	5	PCT-US96-10043-11	Sequence 11, Appli
15	1225	97.2	442	4	US-08-472-888D-7	Sequence 7, Appli
16	1225	97.2	442	5	PCT-US96-10043-9	Sequence 9, Appli
17	1225	97.2	446	3	US-08-397-411-7	Sequence 7, Appli
18	1225	97.2	449	1	US-08-458-516-13	Sequence 13, Appli
19	1225	97.2	459	1	US-08-157-101A-7	Sequence 7, Appli
20	1225	97.2	467	4	US-08-030-175-41	Sequence 41, Appli
21	1225	97.2	467	4	US-08-030-175-42	Sequence 42, Appli
22	1225	97.2	475	4	US-08-740-002-27	Sequence 27, Appli
23	1225	97.2	476	3	US-08-378-939-10	Sequence 20, Appli
24	1225	97.2	476	3	US-08-487-550-4	Sequence 4, Appli
25	1225	97.2	476	3	US-08-487-550-12	Sequence 12, Appli
26	1225	97.2	476	4	US-08-526-098-4	Sequence 4, Appli
27	1225	97.2	476	4	US-08-526-098-12	Sequence 12, Appli

Sequence 4, Appli
 Sequence 12, Appli
 Sequence 8, Appli
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 Sequence 16, Appli
 Sequence 53, Appli
 Sequence 8, Appli
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 Sequence 7, Appli
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 Sequence 2, Appli
 Sequence 7, Appli
 Sequence 33, Appli
 Sequence 3, Appli

ALIGNMENTS

RESULT 1
 US-08-595-043A-50
 Application US/08595043A
 Patent No. 5915824
 GENERAL INFORMATION:
 APPLICANT: SGARLATO, GREGORY D.
 TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
 NUMBER OF SEQUENCES: 90
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MEDLEN & CARROLL
 STREET: 220 MONTGOMERY STREET, SUITE 2200
 CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 COUNTRY: UNITED STATES OF AMERICA
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/595,043A
 FILING DATE: 31-JAN-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: CARROLL, PETER G.
 REGISTRATION NUMBER: 32,837
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 705-8410
 TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 50:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 232 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-595-043A-50
 Query Match Similarity 97.2%; Score 1225; DB 2;
 Best Local Similarity 97.0%; Pred. No. 3.4e-116;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 EPKSCDKTHTCPPCAPELLGGPSVPLFPKPKDTLMISRTPEVYDVSHEPVEKF 60
 Db 1 EPKSCDKTHTCPPCAPELLGGPSVPLFPKPKDTLMISRTPEVYDVSHEPVEKF 60
 61 NNTYDGVEHNVNTKTPREEQYNSTYRVSVSITVHNQWNGKEYKCKVSNKALAPIEKT 120
 61 NWYDGVEHNVAKTKPREEQYNSTYRVSVSITVLEQDWNGKEVKCKVSNKALAPIEKT 120

RESULT 3
 US-09-1178-869-2
 ; Sequence 2, Application US/09178869B
 ; Patent No. 6197294
 ; GENERAL INFORMATION:
 ; APPLICANT: Baetge, E. Edward
 ; APPLICANT: Wong, Shou
 ; APPLICANT: Hickey, William F.
 ; APPLICANT: Hammarskjold, Joseph P.
 ; APPLICANT: Baetge, E. Edward
 ; TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
 ; CURRENT APPLICATION NUMBER: US/09/178,869B
 ; NUMBER OF SEQ ID NOS: 14
 ; LENGTH: 331
 ; SOFTWARE: PatentIn version 2.0
 ; SEQ ID NO: 2
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

Query Match 97.2%; Score 1225; DB 3; Length 331;
 Best Local Similarity 97.0%; Pred. No. 5.6e-116;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCAPELGGPSVLFPPKPKDTLMISRTPETVTVYDVSHEDEPKF 60
 Db 100 EPKSCDKTHTCPPCAPELGGPSVLFPPKPKDTLMISRTPETVTVYDVSHEDEPKF 159

Qy 61 NWYDGVENVKTKPREEQNSTYRVSVLTVLHQNMNGKEYKCKVSNKALPAPTEKT 120
 Db 160 NWYDGVENVKTKPREEQNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPTEKT 219

Qy 121 ISKAKVOPREPOVYTLPSSRDELTKNQVSLLTCLVKGFPDSIAVEWSNGOPENNYKTP 180
 Db 100 EPKSCDKTHTCPPCAPELGGPSVLFPPKPKDTLMISRTPETVTVYDVSHEDEPKF 60

Qy 181 PVLDGSFSFLYSLTKDSSRQGNYFCSVMHEALNHYQRSLSLSPGK 232
 Db 181 PVLDGSFSFLYSLTKDSSRQGNYFCSVMHEALNHYQRSLSLSPGK 232

RESULT 4
 US-09-761-413-2
 ; Sequence 2, Application US/09761413
 ; Patent No. 6506891
 ; GENERAL INFORMATION:
 ; APPLICANT: Tao, Weng
 ; APPLICANT: Wong, Shou
 ; APPLICANT: Hickey, William F.
 ; APPLICANT: Hammarskjold, Joseph P.
 ; APPLICANT: Baetge, E. Edward
 ; TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
 ; FILE REFERENCE: 17810-043
 ; CURRENT APPLICATION NUMBER: US/09/761,413
 ; CURRENT FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US/09/178,869
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 2
 ; LENGTH: 331
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

Query Match 97.2%; Score 1225; DB 4; Length 331;
 Best Local Similarity 97.0%; Pred. No. 5.6e-116;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCAPELGGPSVLFPPKPKDTLMISRTPETVTVYDVSHEDEPKF 60
 Db 100 EPKSCDKTHTCPPCAPELGGPSVLFPPKPKDTLMISRTPETVTVYDVSHEDEPKF 159

Qy 61 NWYDGVENVKTKPREEQNSTYRVSVLTVLHQNMNGKEYKCKVSNKALPAPTEKT 120
 Db 160 NWYDGVENVKTKPREEQNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPTEKT 219

Qy 121 ISKAKVOPREPOVYTLPSSRDELTKNQVSLLTCLVKGFPDSIAVEWSNGOPENNYKTP 180
 Db 120 ISKAKVOPREPOVYTLPSSRDELTKNQVSLLTCLVKGFPDSIAVEWSNGOPENNYKTP 279

Qy 181 PVLDGSFSFLYSLTKDSSRQGNYFCSVMHEALNHYQRSLSLSPGK 232
 Db 180 PVLDGSFSFLYSLTKDSSRQGNYFCSVMHEALNHYQRSLSLSPGK 331

RESULT 5
 US-09-180-100-11
 ; Sequence 11, Application US/09180100
 ; Patent No. 6306395
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAMURA, No. 6306395.io

APPLICANT: NAGATA, Shigekazu
 TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
 FILE REFERENCE: 1110-207P
 CURRENT FILING DATE: US/09/180,100
 EARLIER APPLICATION NUMBER: PCT/JP97/01502
 EARLIER FILING DATE: 1998-11-02
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 11
 LENGTH: 360
 TYPE: PRT
 ORGANISM: Homo sapiens
 -09-180-100-11

Query Match 97.2%; Score 1225; DB 3; Length 360;
 Best Local Similarity 97.0%; Pred. No. 6.3e-116;
 Matches 225; Conservative 3; Mismatches 4; Gaps 0;
 Matches 225; Gaps 0;

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  1 EPKSCDKTHTCPPCAPELGGPSVLFPPKPKDTLMISRTPETVCVVYDVSHEDEPEYKF 60
  129 EPKSCDKTHTCPPCAPELGGPSVLFPPKPKDTLMISRTPETVCVVYDVSHEDEPEYKF 188
  61 NWYVDGVEVNKTKPREEQYNSTYRVSLLTIVLWNGKEYKCKVSNKALPAPIKT 120
  189 NWYVDGVEVNKTKPREEQYNSTYRVSLLTIVLWNGKEYKCKVSNKALPAPIKT 248
  121 ISAKAKVQPREPOVTTLPSPRSDELTKRNQSVLCLVGFYPSDIAVEWSNGOPENNYKTP 180
  249 ISAKAKVQPREPOVTTLPSPRSDELTKRNQSVLCLVGFYPSDIAVEWSNGOPENNYKTP 308
  181 PVLDGSFFFLYSKLTVDSRMRQQNVSFCSCVMSHEALTHYHQRSLSLSPGK 232
  309 PVLDGSFFFLYSKLTVDSRMRQQNVSFCSCVMSHEALTHYHQRSLSLSPGK 360
  
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SULT 6

-08-236-311-7

Sequence 7, Application US/08236311

Patent No. 556535

GENERAL INFORMATION:

APPLICANT: Capon, Daniel J.

APPLICANT: Gregory, Timothy J.

TITLE OF INVENTION: Adheson Variants

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/2336,311

FILING DATE: 02-MAY-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/936190

FILING DATE: 26-AUG-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/842777

FILING DATE: 18-FEB-1992

PRIOR APPLICATION NUMBER: 07/250785

FILING DATE: 28-SEP-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/104329

FILING DATE: 02-OCT-1987

RESULT 7

US-08-236-311-7

Sequence 7, Application US/08457918

Patent No. 6117655

GENERAL INFORMATION:

APPLICANT: Capon, Daniel J.

APPLICANT: Gregory, Timothy J.

TITLE OF INVENTION: Adheson Variants

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/457,918

FILING DATE: 1-JUN-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/236311

FILING DATE: 02-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/842777

FILING DATE: 18-FEB-1992

PRIOR APPLICATION NUMBER: 07/250785

FILING DATE: 28-SEP-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/104329

FILING DATE: 02-OCT-1987

1

ATTORNEY/AGENT INFORMATION:

NAME: Hasak, Janet E.

REGISTRATION NUMBER: 28,616

REFERENCE/DOCKET NUMBER: 444PIC2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1996

TELEFAX: 415/952-9881

TELEX: 910/371-7166

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 371 amino acids

TOPOLogy: linear

US-08-236-311-7

Query Match 97.2%; Score 1225; DB 1; Length 371;
 Best Local Similarity 97.0%; Pred. No. 6.3e-116;
 Matches 225; Conservative 3; Mismatches 4; Gaps 0;

Qy 1 EPKSCDKTHTCPPCAPELGGPSVLFPPKPKDTLMISRTPETVCVVYDVSHEDEPEYKF 60
 Db 140 EPKSCDKTHTCPPCAPELGGPSVLFPPKPKDTLMISRTPETVCVVYDVSHEDEPEYKF 199
 Qy 61 NWYVGVEVNKTKPREEQYNSTYRVSLLTIVLWNGKEYKCKVSNKALPAPIKT 120
 Db 200 NWYVGVEVNKTKPREEQYNSTYRVSLLTIVLWNGKEYKCKVSNKALPAPIKT 259
 Qy 121 ISAKAKVQPREPOVTTLPSSDELTKRNQSVLCLVGFYPSDIAVEWSNGOPENNYKTP 180
 Db 260 ISAKAKVQPREPOVTTLPSSDELTKRNQSVLCLVGFYPSDIAVEWSNGOPENNYKTP 319
 Qy 181 PVLDGSFFFLYSKLTVDSRMRQQNVSFCSCVMSHEALTHYHQRSLSLSPGK 232
 Db 320 PVLDGSFFFLYSKLTVDSRMRQQNVSFCSCVMSHEALTHYHQRSLSLSPGK 371

RESULT 7

US-08-236-311-7

Sequence 7, Application US/08457918

Patent No. 6117655

GENERAL INFORMATION:

APPLICANT: Capon, Daniel J.

APPLICANT: Gregory, Timothy J.

TITLE OF INVENTION: Adheson Variants

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/457,918

FILING DATE: 1-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/236311

FILING DATE: 02-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/842777

FILING DATE: 18-FEB-1992

PRIOR APPLICATION NUMBER: 07/250785

FILING DATE: 28-SEP-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/104329

FILING DATE: 02-OCT-1987

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/104329
 FILING DATE: 02-OCT-1987
 ATTORNEY/AGENT INFORMATION:
 NAME: Kubinec, Jeffrey S.
 REGISTRATION NUMBER: 36,575
 REFERENCE/DOCKET NUMBER: P0444P1C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-8228
 TELEX: 415/952-9881
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 371 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 -08-457-918-7

SEQUENCE Match Score 1225; DB 3; Length 371;
 Best Local Similarity 97.0%; Pred. No. 6..6e-116;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 EPKSCDKTHTCPPCPAPPELGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 140 EPKSCDKTHTCPPCPAPPELGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 199
 61 NWYDGVEVHNATKTPREEQYNSTYRVSVLTIVHQDWLNGKEYCKVSNKALPAPIEKT 120
 200 NWYDGVEVHNATKTPREEQYNSTYRVSVLTIVHQDWLNGKEYCKVSNKALPAPIEKT 259
 121 ISKAKVQPREPVQVTLPPSERDELTKNQSLTVLQGKPSDIAVEWSNGOPENNYKTTP 180
 260 ISKAKGQPQPREPVQTLPPSERDELTKNQSLTVLQGKPSDIAVEWSNGOPENNYKTTP 319
 181 PVLDGSFSFLYSLKLTVDSRQSRQGNYFCSYMHAEIHNHYQQRSHSLSSPGK 232
 320 PVLDGSFSFLYSLKLTVDSRQSRQGNYFCSYMHAEIHNHYTQKSLSLSSPGK 371

SUFT 8
 -10-157-408-7
 Sequence 7, Application US/10157408
 PATENT INFORMATION:
 APPLICANT: Capon, Daniel J.
 TITLE OF INVENTION: Adheson Variants
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/157,408
 FILING DATE: 28-MAY-2002
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/457,918
 FILING DATE: 1-JUN-1995
 APPLICATION NUMBER: 08/236611
 FILING DATE: 02-MAY-1994
 APPLICATION NUMBER: 07/936190
 FILING DATE: 26-AUG-1992
 APPLICATION NUMBER: 07/842777
 FILING DATE: 18-FEB-1992

APPLICATION NUMBER: 07/230785
 FILING DATE: 28-SEP-1988
 APPLICATION NUMBER: 07/104329
 FILING DATE: 02-OCT-1987
 ATTORNEY/AGENT INFORMATION:
 NAME: Kubinec, Jeffrey S.
 REGISTRATION NUMBER: 36,575
 REFERENCE/DOCKET NUMBER: P0444P1C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-8228
 TELEX: 910/371-57168
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 371 amino acids
 TYPE: amino acid
 TOPOLOGY: Linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-10-157-408-7

Query Match Score 1225; DB 4; Length 371;
 Best Local Similarity 97.0%; Pred. No. 6..6e-116;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCPAPPELGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 Db 140 EPKSCDKTHTCPPCPAPPELGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 199
 Qy 61 NWYDGVEVHNATKTPREEQYNSTYRVSVLTIVHQDWLNGKEYCKVSNKALPAPIEKT 120
 Db 200 NWYDGVEVHNATKTPREEQYNSTYRVSVLTIVHQDWLNGKEYCKVSNKALPAPIEKT 259
 Qy 121 ISKAKVQPREPVQVTLPPSERDELTKNQSLTVLQGKPSDIAVEWSNGOPENNYKTTP 180
 Db 260 ISKAKGQPQPREPVQTLPPSERDELTKNQSLTVLQGKPSDIAVEWSNGOPENNYKTTP 319
 Qy 181 PVLDGSFSFLYSLKLTVDSRQSRQGNYFCSYMHAEIHNHYQQRSHSLSSPGK 232
 Db 320 PVLDGSFSFLYSLKLTVDSRQSRQGNYFCSYMHAEIHNHYTQKSLSLSSPGK 371

RESULT 9
 US-09-10-100-22
 Sequence 22, Application US/09180100
 Patent No. 630395
 GENERAL INFORMATION:
 APPLICANT: NAKAMURA, No. 6306395io
 APPLICANT: NAGATA, Shigezaku
 TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE
 FILE REFERENCE: 1110-207P
 CURRENT APPLICATION NUMBER: US/09/180,100
 CURRENT FILING DATE: 1998-11-02
 EARLIER APPLICATION NUMBER: PCT/JP9/01502
 EARLIER FILING DATE: 1997-05-01
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO: 22
 LENGTH: 376
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-180-100-22

Query Match Score 1225; DB 3; Length 376;
 Best Local Similarity 97.0%; Pred. No. 6..8e-116;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCPAPPELGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 Db 145 EPKSCDKTHTCPPCPAPPELGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 204
 Qy 61 NWYDGVEVHNATKTPREEQYNSTYRVSVLTIVHQDWLNGKEYCKVSNKALPAPIEKT 120
 Db 205 NWYDGVEVHNATKTPREEQYNSTYRVSVLTIVHQDWLNGKEYCKVSNKALPAPIEKT 264

SULT 10
-08-784-512-3
Sequence 3, Application US/08784512
Patent No. 5872209
GENERAL INFORMATION:
APPLICANT: BARTNIK, Eckart
APPLICANT: EIDENMUELLER, Bernd
APPLICANT: BUETTNER, Frank
APPLICANT: CATERSON, Bruce
APPLICANT: HUGHES, Clare
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOCS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,512
FILING DATE: 17-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96100682.2
FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/311
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..396

3-00-784-512-3

Query Match 97.2%; Score 1225; DB 2; Length 396;
Best Local Similarity 97.0%; Pred. No. 7.3e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Y 1 EPKSCDKTHCPPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
b 165 EPKSCDKTHCPPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 224
Y 61 NWYDGVEVHNKTKPREEYNSYRVSVLTVLHQNMNGKEYKCKVSNKALPAPIKT 120
b 225 NWYDGVEVHNKTKPREEYNSYRVSVLTVLHQDWNGKEYKCKVSNKALPAPIKT 284

SULT 11
US - 09-176-228-3
Sequence 3, Application US/09176228
Patent No. 6180334
GENERAL INFORMATION:
APPLICANT: BARTNIK, Eckart
APPLICANT: EIDENMUELLER, Bernd
APPLICANT: BUETTNER, Frank
APPLICANT: CATERSON, Bruce
APPLICANT: HUGHES, Clare
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)

CURRENT SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOCS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/176,228
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/784,512
FILING DATE: 17-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/311
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..396

US - 09-176-228-3

Query Match 97.2%; Score 1225; DB 3; Length 396;
Best Local Similarity 97.0%; Pred. No. 7.3e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Y 1 EPKSCDKTHCPPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 165 EPKSCDKTHCPPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 224
Y 61 NWYDGVEVHNKTKPREEYNSYRVSVLTVLHQNMNGKEYKCKVSNKALPAPIKT 120
Db 225 NWYDGVEVHNKTKPREEYNSYRVSVLTVLHQDWNGKEYKCKVSNKALPAPIKT 284

RESULT 13
PCT-US95-03866-14
Sequence 14; Application PC/TUSS9503866
GENERAL INFORMATION:
APPLICANT: Cytomed, Inc. (all states except US)
APPLICANT: Nocka, Karl (US only)
APPLICANT: Lobell, Robert B (US only)
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOCS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03866
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,379
FILING DATE: 28-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: CytoMed/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-03866-12

Query Match 97.2%; Score 1225; DB 5; Length 424;
Best Local Similarity 97.0%; Pred. No. 8e-116; 4; Indels 0; Gaps 0;
Matches 225; Conservative 3; Mismatches 0;

Qy 1 EPKSCDKTHTCPPCPAPELIGGSPVFLFPKPKDLMISRTPETVYDVSHEDPVEKF 60
Db 193 EPKSCDKTHTCPPCPAPELIGGSPVFLFPKPKDLMISRTPETVYDVSHEDPVEKF 252

Qy 61 NWYDGVEHNVKTKPREEQNSTYRVSVLTVLHQWNGKEYKCKVSNKALPAPIKT 120
Db 253 NWYDGVEHNVKTKPREEQNSTYRVSVLTVLHQWNGKEYKCKVSNKALPAPIKT 312

Qy 121 ISKAKVQPEPQVTLPPRDELTKQVSLTCLVKGPSPSDIAVEMSGOPENNYKTTP 180
Db 313 ISRKKGQPREPVYTLPPRDELTKQVSLTCLVKGPSPSDIAVEMSGOPENNYKTTP 372

Qy 181 PVLDVGSSFFLYSKLTVDKSRWQGNFSCSYMEHALNHYQQRSLSLSPGK 232
Db 373 PVLDGSSFFLYSKLTVDKSRWQGNFSCSYMEHALNHYTOKSLSLSPGK 424

Qy 121 ISKAKVQPEPQVTLPPRDELTKQVSLTCLVKGPSPSDIAVEMSGOPENNYKTTP 180
Db 313 ISRKKGQPREPVYTLPPRDELTKQVSLTCLVKGPSPSDIAVEMSGOPENNYKTTP 372

Qy 181 PVLDVGSSFFLYSKLTVDKSRWQGNFSCSYMEHALNHYQQRSLSLSPGK 232
Db 373 PVLDGSSFFLYSKLTVDKSRWQGNFSCSYMEHALNHYTOKSLSLSPGK 424

RESULT 14
PCT-US96-10043-11
Sequence 11; Application PC/TUSS9610043
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: p-SELECTIN LIGANDS AND RELATED MOLECULES

TITLE OF INVENTION: AND METHODS
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0.1, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/10043
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA: US 60/000,213
 APPLICATION NUMBER: 00786/284001
 FILING DATE: 14-JUN-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Lechi, Karen F.
 REGISTRATION NUMBER:
 REFERENCE/DOCKET NUMBER: 00786/284001
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 TELEX: 200154
 SEQUENCE CHARACTERISTICS:
 LENGTH: 437 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 T-US96-10043-11

Query Match 97.2%; Score 1225; DB 5; Length 437;
 Best Local Similarity 97.0%; Pred. No. 8.4e-116;
 Matches 225; Conservative 4; Mismatches 0; Gaps 0;
 1 EPKSCDKTHTCP CPPC PAPELLGGPSVLFPPPKPDKTLMISRPTPEVYKPF 60
 206 EPKSCDKTHTCP PAPELLGGPSVLFPPPKPDKTLMISRPTPEVYKPF 265
 61 NWYDGVEHNWKTKPREEQNSTYRVSITLVHONMNGKEYKCKVSNKALPAPIEKT 120
 266 NWYDGVEHNWKTKPREEQNSTYRVSITLVHONLNGKEYKCKVSNKALPAPIEKT 325
 121 ISAKYQPREEPVYTLPPSRDELTKNQVSLTCLYRGFYPSDIAVEWENGQPNNYKTP 180
 326 ISAKYQPREEPVYTLPPSRDELTKNQVSLTCLYRGFYPSDIAVEWENGQPNNYKTP 385
 181 PVLDVGSSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYOORSLSLSPGK 232
 386 PVLDGSSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQSKTSLSLSPGK 442

Search completed: October 27, 2004, 17:05:53
 Job time : 24.1174 sec

RESULT 15
 3-08-472-888A-7
 Sequence 7, Application US/08472888A
 Patent No. 661376

GENERAL INFORMATION:
 APPLICANT: Seed, Brian

APPLICANT: Walz, Gerd
 TITLE OF INVENTION: AGP-ANTIBODY FUSION PROTEINS
 TITLE OF INVENTION: AND RELATED MOLECULES AND METHODS
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Clark & Ebbing LLP
 STREET: 116 Federal Street

CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/472, 888A
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/618, 314
 FILING DATE: 23-NOV-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Ebbing, Karen L.
 REGISTRATION NUMBER: 35.238
 REFERENCE/DOCKET NUMBER: 00786/258001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-428-0200
 TELEFAX: 617-428-7045
 TELEX:
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 442 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-472-888A-7

Query Match 97.2%; Score 1225; DB 4; Length 442;
 Best Local Similarity 97.0%; Pred. No. 8.5e-116;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 EPKSCDKTHTCP CPPC PAPELLGGPSVLFPPPKPDKTLMISRPTPEVYKPF 60
 Db 211 EPKSCDKTHTCP CPPC PAPELLGGPSVLFPPPKPDKTLMISRPTPEVYKPF 270
 Qy 61 NWYDGVEHNWKTKPREEQNSTYRVSITLVHONMNGKEYKCKVSNKALPAPIEKT 120
 Db 271 NWYDGVEHNWKTKPREEQNSTYRVSITLVHONLNGKEYKCKVSNKALPAPIEKT 330
 Qy 121 ISAKYQPREEPVYTLPPSRDELTKNQVSLTCLYRGFYPSDIAVEWENGQPNNYKTP 180
 Db 331 ISAKYQPREEPVYTLPPSRDELTKNQVSLTCLYRGFYPSDIAVEWENGQPNNYKTP 390
 Qy 181 PVLDVGSSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYOORSLSLSPGK 232
 Db 391 PVLDGSSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQSKTSLSLSPGK 442

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GenCore version 5.1.6
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4 protein - protein search, using sw model

in on: October 27, 2004, 16:51:09 ; Search time 28.7722 Seconds
(without alignments)

1103.547 Million cell updates/sec

title: US-10-000-439-2

erfect score: 174

sequence: 1 ASTRGSPVPLAPSSKSTSG.....MHEBALHNHYQQRSLSLSPGK 330

scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 283416 seqs, 96216763 residues

otal number of hits satisfying chosen parameters:

283416

imum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase : PIR_79;*

1: D1rl;*

2: pi2;*

3: pi3;*

4: pi4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Length	DB ID	Description
1	1729	98.0	330 1 GHHU	Ig gamma-1 chain C
2	1592.5	90.3	377 2 A23511	Ig gamma-3 chain C
3	1590.5	90.2	377 2 A60764	Ig gamma-3 chain C
4	1566	89.8	326 1 G2HU	Ig gamma-2 chain C
5	1552.5	88.0	327 1 G4HU	Ig gamma-4 chain C
6	1225.5	69.5	374 2 S693319	Ig heavy chain V r
7	1222	69.4	328 2 I47159	Ig gamma-2a chain C
8	1222	69.3	255 4 S31866	Ig gamma-1 chain C
9	1219	69.1	328 2 I47160	Ig gamma-2b chain
10	1216	68.9	234 2 PT0287	Ig gamma chain C r
11	1193	67.6	328 2 I47138	Ig gamma-1 chain C
12	1192	67.5	323 1 GHR13	Ig gamma chain C r
13	1189	67.4	328 2 I47161	Ig gamma-3 chain C
14	1174.5	66.6	329 1 G2GP	Ig gamma-2 chain C
15	1163.5	66.0	472 2 S31459	Ig gamma-1 chain C
16	1144.5	64.9	470 2 S22080	Ig heavy chain pre
17	1125.5	63.8	308 2 C30554	Ig heavy chain C r
18	1123	63.7	289 1 G3H0WI	Ig gamma-3 heavy C
19	1117.5	63.4	333 2 PS0019	Ig gamma-2b chain monoclonal antibody
20	1116	63.3	444 2 PC4416	Ig gamma-1 chain C
21	1114	63.2	326 2 PS0017	Ig gamma-1 chain C
22	1109	62.9	324 1 G1MS	Ig gamma-3 chain C
23	1108	62.8	329 1 G3MS	Ig gamma-1 chain C
24	1104	62.6	393 1 G1MSM	Ig gamma-3 chain C
25	1097	62.2	398 1 G2MSM	Ig gamma-2a chain
26	1093	62.0	330 1 G2MSA	Ig gamma-2a chain
27	1093	62.0	459 2 S37483	Ig gamma-2a chain
28	1090.5	61.8	335 1 G2MSAB	Ig gamma-2a chain
29	1088	61.7	399 1 G2MSM	Ig gamma-2a chain

RESULT 1

GHHU

Ig gamma-1 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 31-Jan-1981 #Sequence revision 18-Aug-1982 #text_change 09-Jul-2004

C;Accession: A93433; S33887; B90563; A90564; B91668; A91723; A02146

R;Fillion, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A;Title: The nucleotide sequence of a human immunoglobulin C-gamma gene.

A;Reference number: A93433; MUID: 82274238; PMID: 6287432

A;Accession: A93433

A;Molecule type: DNA

A;Residues: 1-330 <ELL>

A;Cross-references: UNIPROT: P01857; EMBL: Z11370

A;Note: this sequence has the Glm(17) allotype marker,

A;Note: Lys-330 is removed after translation

R;Harris, L.J.

submitted to the EMBL Data Library, October 1992

A;Reference number: S33904

A;Accession: S336801

A;Molecule type: DNA

A;Residues: 2-330 <HAB>

R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Honjo, T.

Cell 29, 671-679, 1982

A;Title: Structure of a human immunoglobulin gamma genes: implications for evolution of a

A;Reference number: S33887; MUID: 830301943; PMID: 6811139

A;Accession: S33887

A;Molecule type: DNA

A;Cross-references: EMBL: Z17370

R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Maxdal, M.J.; Edelman, C.

Biochemistry 9, 3161-3170, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequenc

A;Reference number: A0563; MUID: 71064024; PMID: 548977

A;Contents: myeloma protein Eu

A;Accession: B90563

A;Molecule type: protein

A;Residues: 1-96, R, 98-135 <CUN>

A;Note: this sequence has the Glm(3) marker, 97-Arg

R;Rutishauser, U.; Cunningham, B.A.; Bennett, G.M.

Biochemistry 9, 3171-3181, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequenc

A;Reference number: A0564; MUID: 71064025; PMID: 5530842

A;Contents: Bu

A;Accession: A90564

A;Molecule type: protein

A;Residues: 136-154, Q, 155-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240, '

R;Ponding, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A;Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

:20-85/Domain: immunoglobulin homology <IMM>

Query Match 90.2%; Score 1590.5; DB 2; Length 377;
 Best Local Similarity 80.1%; Pred. No 1;le-102; A:Residues: 238-275 <HOF>
 Matches 302; Conservative 13; Mismatches 15; Indels 47; Gaps 1;
 A:Accession: A93132
 A:Molecule type: protein
 A:Reference number: A94591
 A:Contents: annotation; zle; revisions to residues 25, 59, 60, and 264-268
 A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic
 ne
 R.Milstein, C.; Frangione, B.
 Biochem. J. 121: 217-225, 1971.
 A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
 A:Reference number: A90254; MUID: 2033500; PMID: 940472
 A:Contents: annotation; myeloma protein; Sa, disulfide bonds
 R;Frangione, B.; Milstein, C.; Pink, J.R.L.
 Nature 221, 145-148, 1969
 A:Title: Structural studies of immunoglobulin G.
 A:Reference number: A93157; MUID: 61064124; PMID: 5782707
 A:Contents: annotation; Sa, disulfide bonds
 A:Gene:IGHG2
 A:Cross references: GDB:119338; OMIM:147110
 A:NP: Position: 14q32.33-4q33.33
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (Kappa) chains disulfide bonded. In some cases, such as IgA and IgM, the subunits associate into 1α1
 C:Superofamily: Immunoglobulin C region; immunoglobulin homology
 C:Superfamily: duplication; Glycoprotein; heterotetramer; immunoglobulin F:20-85/Domain: immunoglobulin homology <IM>
 F:1-13/Domain: immunoglobulin homology <IM3>
 F:139-306/Domain: immunoglobulin homology
 F:14/Disulfide bonds: interchain (to light chain) #status experimental
 F:21-83,140-200,246-304/Disulfide bonds: #status experimental
 F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
 F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

RESULT 4

2HU gamma-2 chain C region - human
 ;Species: Homo sapiens (man)
 ;Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 09-Jul-2004
 ;Accession: A93906; MUID: 29809; A93122; A02148
 ;Ellison, J.; Hood, L.
 ;Wang, A.C.; Tung, E.; Rudenberg, H.H.
 ;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
 ;Reference number: A93906; MUID: 82197621; PMID: 6804948
 ;Accession: A93906
 ;Molecule type: DNA
 ;Residues: 1-326 <ELL>
 ;Cross-references: UNIPROT: P01859; GB:V00554; GB:J00230; PIDN: 932759; NID: 932759; P
 ;Note: Lys-326 is probably removed Post-translationally
 ;Wang, A.C.; Tung, E.; Rudenberg, H.H.
 ;Immunol. Rev., 128, 104-1054, 1980
 ;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
 ;Reference number: A92809; MUID: 81007873; PMID: 6774012
 ;Accession: A92809
 ;Molecule type: protein
 ;Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
 ;Note: Trp-156 is at or near the complement-binding site
 ;Connell, G.E.; Parr, D.M.; Hofmann, T.
 ;Title: The amino acid sequences of the three heavy chain constant region domains of a
 ;Reference number: A90752; MUID: 80001357; PMID: 113060
 ;Contents: myeloma protein Zle
 ;Accession: A90752
 ;Molecule type: protein
 ;Residues: 1-24, 'E', 26-57
 ;Note: this sequence has since been revised
 ;Hofmann, T.; Parr, D.M.
 ;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
 ;Reference number: A93132; MUID: 80114419; PMID: 118920
 ;Contents: Zle

RESULT 5

G4HU
 Ig Gamma-4 chain C region - human
 ;Species: Homo sapiens (man)
 ;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
 ;Accession: A90241; MUID: 212150
 ;R;Ellison, J.; Buxbaum, J.; Hood, L.
 ;DNA 1-11-18, 1981
 A;Title: Nuc-eotide sequence of a human immunoglobulin C-gamma4 gene.

A;Reference number: A90933 ; MUID:83157104 ; PMID:6299662
A;Accession: A90933
A;Molecule type: DNA
A;Residues: 1-327 <ELL>
A;Cross-references: UNIPROT:P01861
A;Note: The sequence was determined from the germline gene
R;Pink, J.R.L.; Buttry, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant region
A;Reference number: A90249 ; MUID:70207560 ; PMID:4192659
A;Accession: A90249
A;Molecule type: protein
A;Residues: 1-30-81-1-266 <PIN>
A;Genetics:
A;Gene: GDB:IGRG4
A;Cross-references: GDB:1193440 ; OMIM:147130
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (κ) chains disulide bonds. In some cases, such as IgA and IgM, the subunits associate into a C-Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F; 20-85; Domain: immunoglobulin homology <IM2>
F;99-110/Region: hinge
F;134-203/Domain: immunoglobulin homology <IM2>
F;240/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83; 141-201; 247-305/Disulfide bonds: #status predicted
F;106; 109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 88.0%; Score 1552.5; DB 1; Length 327;
Best Local Similarity 88.0%; Pred. No. 3.8e-100; Indels 3; Gaps 1;
Matches 293; Conservative 15; Mismatches 19; Indels 8; Gaps 1;
Db 1 ASTKGPSVFPALAPSSGSGTAAAGCLVKDLYFPBPVTVSWNSALTSGVHPPAVQLOSS 60
1 ASTKGPSVFPALARCSRTSEAAALCIVKDVYFPBPVTVSWNSALTSGVHPPAVQLOSS 60
RESULT 7
I47159
Ig Gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47159
R;Kacskovics, I.; Sun, J.-J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a :
A;Reference number: 95015845 ; PMID:7930579
A;Accession: I47159
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residue: 1-328 <KAC>
A;Cross-references: EMBL:U03779 ; NID:9433123 ; PID:9433124
C;Genetic info:
A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology <IM2>
F;133-202/Domain: immunoglobulin homology <IM2>
Query Match 69.4%; Score 1225; DB 2; Length 328;
Best Local Similarity 67.5%; Pred. No. 1.7e-77; Indels 6; Gaps 2;
Matches 224; Conservative 46; Mismatches 56;
Db 1 ASTKGPSVFPPLAPS SKSTSGGTAAALGCLVKDLYFPBPVTVSWNSALTSGVHPPAVQLOSS 60
1 APKAPASPYPLAPSRDTSRDPNVALGCLASSYFPEPVTVWNGLASSGHTFPBVQLQBS 60
Db 61 GLYLSISSVTVPSSSLGQTQYCNVNEHKPSNTKVDKKEPKSCDTHTCPPCPAELGG 120
61 GLYLSISSVTVPSSSLKSYTCVNVEHPATTKVDRVGKTKPCCPICPACESP----G 116
Db 121 PSVTFPPKPKDPTMISRTPEVTCVVVDVSHEDPEVFKNWVVDGEVEVANVKTKEPEEQVN 180
Db 118 PSVTFPPKPKDPTMISRTPEVTCVVVDVSDQEPVQFWYVDEVEVAKTKPREFQVN 177
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSKNSKALPAPIEKTSKAKWQPREQVYTLPPSRDE 240
Db 178 STYRVSVLTVLHQDWLNGKEYKCKVSKNSKALPSSIEKTISKAKCQPREQVYTLPPQEE 237
Db 241 LTKNOVSLTCLVKGFPSVDAVEWENQGPENNYKTPVYDLSGSFLYSLKLTVDCSR 300
Db 238 MTKNOVSLTCLVKGFPSVDAVEWENQGPENNYKTPVYDLSGSFLYSLRJTVDCSRW 297
Db 301 QQQNFSVSSVMEALLNHYQORSLSLSPGK 330
Db 298 QEGNFSVSSVMEALLNHYQKSLSLSPGK 327
RESULT 6
S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Dte: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
R;Khamlichchi, A.A.; Autourier, P.; Preud'homme, J.-L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339 ; MUID:95262687 ; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA

Query Match 69.1%; Score 1219; DB 2; Length 328;
 Best Local Similarity 67.2%; Prid. No. 4.3e-77;
 Matches 223; Conservative 45; Mismatches 58; Indels 6; Gaps 2;

1 ASTKQPSVPLAPSSKSTSGCTTALGCLVKDYKPEPEVTVWSNIGALTSGVHTFPAVLOSS 60
 1 APKTAPLVPLAPCERDTGPNTVALGCLASSYPEPVTVTWSNIGALTSGVHFPSV1QPS 60

241 LTKVQSLTCLVYKGFPSPDSAVEWESNGQ - PENNYKTRTPPVLSVGSEFLSRLTVDS 298
 237 LSRSKVSLTCLVGFPPDIDVWRNGQPEPGNYRTTPQQDVDGTYFLYSKSFVDKA 296

299 RQGQHNFCSYMSMHEALTHNHYQORSLSLSPGK 330

297 SWGGGGFQCAVMHEALTHNHYTQKSISKPK 328

SPLIT 8

1866 Gamma-1 chain C region - synthetic
 Species: synthetic
 Note: Homo sapiens (man) Gene engineered and expressed in Escherichia coli
 Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
 Filipula, D.
 Submitted to the EMBL Data Library, February 1993
 Description: Screening method for protein-protein interactions of cloned gene products.
 Reference number: S31866
 Molecule type: mRNA
 Residues: 1-255 <FILE>
 Cross references: EMBL:X70421; NID:933068; PIDN:CAA49866_1; PID:933069

23-25/Region: Escherichia coli outer membrane protein A precursor
 23-25/Region: human Ig gamma-1 chain C region

Query Match 69.3%; Score 1222; DB 4; Length 255;
 Best Local Similarity 94.6%; Prid. No. 2e-77;
 Matches 226; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

92 TKVDKVKVPKSCDKTHTCPPCPKPDITLMSRTPETVTVYDVS 151
 17 TVQADVESKSCDKTHTCPPCPKPDITLMSRTPETVTVYDVS 76

152 EDPVVKENWYDGVENAKTRKPREEQYNSTTVSVLTVIHQDNMNGKEYKCKVSNKAL 211
 77 EDPEVKENWYDGVENAKTRKPREEQYNSTTVSVLTVIHQDNMNGKEYKCKVSNKAL 136

212 PAPEKTIKAKYQPREPOVTLPPSDELTNQVSITCLYKGFYPSDIAVEWENGQPE 271
 137 PAPEKTIKAKGQPREPOVTLPPSDELTNQVSITCLYKGFYPSDIAVEWENGQPE 196

272 NYKXKTPTPVLDGSFELSYFLSKLTVDKSRWQOGNFSCSVMEALTHNHYQORSLSLSPGK 330
 197 NYKXKTPTPVLDGSFELSYFLSKLTVDKSRWQOGNFSCSVMEALTHNHYTQKSISLSPGK 255

RESULT 9

17160 3 gamma 2b chain constant region - pig (fragment)
 ;Species: Sus scrofa domestica (domestic pig)
 ;Accession: I47160
 ;Immunol. 153, 3565-3573, 1994
 ;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a single immunoglobulin gene
 ;Reference number: I47158; MUID:95015845;
 ;Accession: I47160
 ;Status: preliminary; translated from GB/EMBL/DDBJ
 ;Molecule type: mRNA
 ;Residues: 1-128 <KAC>
 ;Cross-references: EMBL:U03780; NID:9433125; PIDN:AA52218_1; PID:9433126

147158 Ig gamma 1 chain constant region - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)
 ;Gene: IgG2b
 ;Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>
 ;133-202/Domain: immunoglobulin homology <IMM>

RESULT 11

147159 Ig gamma 1 chain constant region - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)
 ;Gene: IgG2b
 ;Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>

C;Accession: I47158

21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

Db 1 PENNYKTRTPVLDGSFELSYFLSKLTVDKSRWQOGNFSCSVMEALTHNHYQORS 323
 Db 181 PENNYKTRTPVLDGSFELSYFLSKLTVDKSRWQOGNFSCSVMEALTHNHYTQKS 234

Db 150 SHEDPEVKENWYDGVENAKTRKPREEQYNSTTVSVLTVIHQDNMNGKEYKCKVSNKAL 209
 Db 61 SHEDPEVKENWYDGVENAKTRKPREEQYNSTTVSVLTVIHQDNMNGKEYKCKVSNKAL 120

Db 210 ALAPIEKTISKAKVQPREPOVTLPPSDELTKNQVSITCLYKGFYPSDIAVEWENGQ 269
 Db 121 ALAPIEKTISKAKVQPREPOVTLPPSDELTKNQVSITCLYKGFYPSDIAVEWENGQ 180

Db 270 PENNYKTRTPVLDGSFELSYFLSKLTVDKSRWQOGNFSCSVMEALTHNHYQORS 323
 Db 181 PENNYKTRTPVLDGSFELSYFLSKLTVDKSRWQOGNFSCSVMEALTHNHYTQKS 234

R.; Racskovics, I.; Sun, J.; Butler, J.E.
 J. Immunol. 153, 3565-3573, 1994
 A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
 A;Accession: I47158; MUID:9501585; PMID:7930579
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Residues: 1-328 <RAC>
 A;Cross-references: EMBL:U03778; NID:9433121; PID:9433122
 C;Genetics:
 A;Gene: IgG1
 C;Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>
 F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 67.6%: Score 1193; DB 2; Length 328;
 Best Local Similarity 67.2%; Pred. No. 2.7e-75;
 Matches 223; Conservative 42; Mismatches 61; Indels 6; Gaps 3;

Qy 1 ASTKGPSVYFPLAPSSKSTSGTAALCIVDYEPPDVTVWSNSALITGGVHPFPANVQSS 60
 Db 1 APKTAPESTYPLAPCGDVSGPNAVACCLASSYFPEPVTVWNNSALITSGVHTPSVQPS 60
 Qy 61 GHYSLSVVTVTPSSSGTQTYICNNHKPNTKYDKVKEPKSDKTHTCPPCAPELGG 120
 Db 61 GLYSLSMMVTPASSLSSKSYTCKVHHPATTKYDKV --GIIHQPCQPTCPGCE VAG 116
 Qy 121 PSVFLFPKPKPDLMMSRTPEVTVWVDSHEDPEVKENWYDGVETVHNKTPREEQYN 180
 Db 117 PSVFLFPKPKPDLMMSQTPEVTVWVDSHEDPEVKENWYDGVETVHNKTPREEQFN 176
 Qy 181 STYRVSVLTVLHOMMNGKEYKCKVSNKALPAPIEKTSKAKVQPREPOQYTLPPRDE 240
 Db 177 STYRVSVLTVLHOMMNGKEYKCKVSNKALPAPIEKTSKAKVQPREPOQYTLPPRDE 236
 Qy 241 LTKNOVSLTCLVKGFPSPDIAVENNSNGO - PENNYKTPTPVLDVGSSFEFLYSKLTVDKS 298
 Db 237 LSRSKVLTCLVIGFPDPDTHVENSNGOPEPENTYRTPQQDVDTENFFYLSKAVIDKA 296
 Qy 299 RWQOGNWFSCSYMMHEALHNHYQQRSLISLSPGK 330
 Db 297 RWDHGDKFECAMHEALHNHYTQKSISKTQGK 328

RESULT 12
 GHRB
 Ig gamma chain C region - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Accession: A91749; A90290; A93928; A90245; A94416; A02161
 Immunogenetics 18, 387-397, 1983
 A;Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplot
 A;Reference number: A91749; MUID:84030930; PMID:6313520
 A;Accession: A90290
 A;Molecule type: mRNA
 A;Residue: 1-323 <BER>
 A;Cross-references: UNIPROT:D01870
 C;Species: Sus scrofa domestica (domestic Pig)
 C;Accession: I47161
 R;Pratt, D.M.; Mole, L.E.
 Biochem. J. 151, 337-349, 1975
 A;Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglobulins
 A;Reference number: A90290; MUID:76155469; PMID:1243651
 A;Accession: A90290
 A;Molecule type: protein
 A;Residues: 1-47, B'-49-71, 'PV'-'72-128 <PRA>
 R;Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
 Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
 A;Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain
 A;Reference number: A93928; MUID:83299917; PMID:6193512
 A;Accession: A93928
 A;Molecule type: mRNA
 A;Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186-'E', 188-266 <MAR>
 A;Cross-references: GB:MB16426; NID:9165111; PID:9165112

RESULT 13
 I47161
 Ig gamma 3 chain constant region - pig (fragment)
 C;Species: Sus scrofa domestica (domestic Pig)
 C;Accession: I47161
 R;Kacskovics, I.; Sun, J.; Butler, J.E.
 J. Immunol. 153, 3565-3573, 1994
 A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
 A;Reference number: I47161
 A;Accession: I47161
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-328 <RAC>
 A;Cross-references: EMBL:U03781; NID:9433127; PID:9433128
 C;Genetics:
 A;Gene: IgG3
 C;Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>
 F:133-202/Domain: immunoglobulin homology <IMM>

Query Match Simillarity 67.4%; Score 1189; DB 2; Length 328;
 Best Local Matches 66.3%; Pred. No. 5.1e-75; Gaps 3;
 Matches 222; Conservative 43; Mismatches 61; Indels 6; Gaps 3;

1 ASTKGPSVPLAPSISKTSGGTAALGCLVKDYFPPPTVSWNSGALTSGVHTPAVLOSS 60
 1 APTAPSYPPLAPCGRDTSQVNLQCLASSYFPPTVMTNSGALTSGVHTPAVLOSS 60
 61 GLYSLSVVTVPSLIGTGTQTYICNWKPSNTKVDKXKEPKSCDKTHTCPPCAPELLGG 120
 61 GLYSLSVVTVPSLSSKSYTCNNHNPATTKVDRVGTKT---KPPCPICOC-E-VAG 116
 121 PSVTFPPKPKPDTLMSITPQTEVYVDPPEVKENMYVDGEEVNVKTPREECQN 180
 117 PSVTFPPKPKPDTLMSITPQTEVYVDPGEVTHAETRQEQQN 176
 181 STYRVVSVLTVLHQUNNGNGKEYKCKVSKNKA LPAPLEKTISKAKYQPREQVYTLPPSDE 240
 177 STYRVVSVLPIQDNLKGKEKCKVNNVNDLPA PTTKIAGGSRREPQVYTLPPABE 236
 241 LTKNQVSLLTCLVKGPYPSDIAVEWESNG--PENNYYKTPPPVLDVGSGFPLYSKLTVDKS 298
 237 LSRSKVTVCLVIGFPDPIHWEKNSGQPEPGNRTTPQODDGTFLYSLKAVDKA 296
 299 RWGQNVYPSCSVHEALTHNHYQRSLLSPGK 330
 297 RWDHGETFECAVNHEALTHNHYTOKS-SKTOGK 328

SULT 14
 GP gamma-2 chain C region - guinea pig
 Species: *Cavia porcellus* (guinea pig)
 Date: 07-May-1995 #sequence_revision 07-May-1981 #text_change 09-Jul-2004
 Accession: A94532; A90359; A90384; A90385; A02151
 Trischmann, T.M.
 Submitted to the Atlas, April 1975
 Reference number: A94553
 Accession: A94533
 Molecule type: Protein
 Residues: 1-3 <TRI>
 Cross references: UNIPROT: P01862
 Biochemistry 10, 18-25, 1971
 Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Amide residues
 Reference number: A90359; MUID: 55338606
 Accession: A90352
 Molecule type: Protein
 Residues: 4-68 <TRI>
 Turner, K.J.; Cebrä, J.J.
 Biochemistry 10, 9-17, 1971
 Title: Structure of heavy chain from strain 13 guinea pig IgG2 antibodies.
 Reference number: A90359; MUID: 55338616
 Accession: A90384
 Molecule type: Protein
 Residues: 134-226 <TRI>
 Trischmann, T.M.; Cebrä, J.J.
 Biochemistry 13, 4804-4811, 1974
 Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
 Reference number: A90385; MUID: 4603467
 Accession: A90385
 Molecule type: protein
 Residues: 227-311 <TR2>
 Olchemirra, B.; Lam, M.E.
 Biochemistry 10, 26-31, 1971
 Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.

A;Reference number: A90354; MUID: 71038474; PMID: 4922544
 A;Contents: annotation; disulfide bonds
 A;Note: Cys-16 is involved in a heavy-light chain bond
 A;Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
 C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a complex.
 C;Keywords: immunoglobulin C region; immunoglobulin homology
 C;Supfamily: immunoglobulin; Glycoprotein; heterotetramer; immunoglobulin
 F;135 204/Domain: immunoglobulin homology <IM1>
 F;241-10/Domain: immunoglobulin homology <IM3>
 F;287-79/Disulfide bonds: #status experimental
 F;142-202/Disulfide bonds: #status experimental
 F;178/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F;248-308/Disulfide bonds: #status experimental
 F;248-308/Disulfide bonds: #status experimental
 Query Match 66.6%; Score 1174.5; DB 1; Length 329;
 Best Local Similarity 66.2%; Pred. No. 5.2e-74; Mismatches 66; Indels 9; Gaps 4;
 Matches 227; Conservative 31; Mismatches 66; Indels 9; Gaps 4;
 Qy 1 ASTKGPSVPLAPSISKTSGGTAALGCLVKDYFPPPTVSWNSGALTSGVHTPAVLOSS 60
 Db 2 ARTTAAASVFLASCDTTSMMTGLCYLKGYFDEPVTKWNNSGALTSGVHTPAVLOSS 60
 Qy 61 GLYSLSVVTVPSLSSGKTYICNWKPSNTKVDKXKEPKSCDKTH---TCPGPCAPPJL 118
 Db 61 GLYSLSVVTVPSLSSGKTYICNWKPSNTKVDKXKEPKSCDKTH---TCPGPCAPPJL 116
 Qy 61 GLYSLSVVTVPSLSSGKTYICNWKPSNTKVDKXKEPKSCDKTH---TCPGPCAPPJL 118
 Db 61 GLYSLSVVTVPSLSSGKTYICNWKPSNTKVDKXKEPKSCDKTH---TCPGPCAPPJL 116
 Qy 119 GCPGVFLFPPKPKDTLMSITPTEVYVDSHEDPEVYFKNWYDGVAVHNVTKPRBQ 178
 Db 117 GCPGVFLFPPKPKDTLMSITPTEVYVDSHEDPEVYFKNWYDGVAVHNVTKPRBQ 176
 Qy 179 YNSTYRVVSVLTVLHQUNNGNGKEYKCKVSKNKA LPAPLEKTISKAKYQPREQVYTLPPSR 238
 Db 177 YNSTYRVVSVLTVLHQUNNGNGKEYKCKVSKNKA LPAPLEKTISKAKYQPREQVYTLPPSR 236
 Qy 239 DELTKQVSLLTCLVKGPYPSDIAVEWESNGP--ENNYKTPYLDSTGSFFFLYSKLVTD 295
 Db 237 DELSKSKVSVLNFPAIDHVWASRNPVSEKEYKNTTPPIEDADGSFYFLYSKLVTD 296
 Qy 297 KSRWQQNVPSGSVMEBALINHYQRSLSLSPG 329
 Db 297 KSRWQQNVPSGSVMEBALINHYQRSLSLSPG 329
 RESULT 15
 S31459
 Ig gamma-1 chain - sheep (fragment)
 C;Species: *Ovis ammon aries* (domestic sheep)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
 C;Accession: S31459
 R;Fatri, S.; Nau, F.
 Submitted to the EMBL Data Library, December 1992
 A;Reference number: S31459
 A;Accession: S31459
 A;Status: preliminary
 C;Species: *Ovis orientalis aries*
 A;Molecular type: mRNA
 A;Residues: 1-472 <PAT>
 A;Cross references: EMBL:X69797
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: immunoglobulin
 F;277-346/Domain: immunoglobulin homology <IMM>
 Query Match 66.0%; Score 1163.5; DB 2; Length 472;
 Best Local Similarity 65.7%; Pred. No. 4.7e-73; Mismatches 71; Indels 3; Gaps 2;
 Matches 218; Conservative 40; Mismatches 71; Indels 3; Gaps 2;
 Qy 1 ASTKGPSVPLAPSISKTSGGTAALGCLVKDYFPPPTVSWNSGALTSGVHTPAVLOSS 60
 Db 142 ASTTPPKYPLTSCCGDTSSSIVTGLCVSSNTKVDKXKEPKSCDKTHCPCAPELLGG 60
 Qy 61 GLYSLSVVTVPSLSSGKTYICNWKPSNTKVDKXKEPKSCDKTHCPCAPELLGG 60

Thu Oct 28 05:36:46 2004

us-10-000-439-2.rpr

Page 8

Db 202 GIYSLSSVVTVPASTGAGCPICNVAPASSTKVDKRVEPGCCPPCXCIC-RCPPEPLPGG 260
Qy 121 PSVFLPPPKPKDTLMISRTPETCYVVDYSHEDPEVKENWYDGEVEVNKTCKPREEQYN 180
Db 261 PSVFIIFPKPKDTLTSGTPTVTCVVDGQDDBQFWFVNVERTARTKPREEQFN 320
Qy 181 STYRVYSLVLTIVHOMMANGKEYKCKXSNKALPAPIEKNTISKAATQPRBPQVYTLPPRDE 240
Db 321 STFRVVSALPIQHQDWTTGGKEFKCRVNEALPAPVRTRISRTKGQAESPQVYLAPOQEE 380
Qy 241 LTKNQSLITCLVKGFPSPDAVENEWSNGP-ENYKTTPPVLDSVSSEFLYSKLTVDKS 298
Db 381 LSKSTLUSVTCLVTGFPDYIAVENEWSNGQPESEDKYGTTSQDADGSYFLYSRLRVDKN 440
Qy 299 RWQGNVFSCVVMHEALHNXYQQSLSLSPGK 330
Db 441 SWOEGDTYACVVMHEALHNHYTQKSISKSFGK 472

Search completed: October 27, 2004, 17:04:50

Job time : 30.2722 secs

GenCore version 5.1.6
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1 protein - protein search, using sw model

in on: October 27, 2004, 16:32:53 ; Search time 149.733 Seconds
 (without alignments)
 1268.081 Million cell updates/sec

title: US-10-000-439-2

infect score: 1764

evidence: 1 ASTRGPSPVPLAPSSKSTSG..... MHEALHNHYQQRSLISLSPGK 330

oring table: BLASTM62
 Gapop 10.0 , Gapext 0.5

searched: 1825181 seqs, 575374646 residues

total number of hits satisfying chosen parameters: 1825181

minimum DB seq length: 0
 maximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

itabase : UniProt_02:
 1: uniprot_sprot:
 2: uniprot_trembl:
 * [4]

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

#	Query	Score	Match	Length	ID	Description
1	Aah14258	98.0	330	1	GCI_HUMAN	P01857 homo sapien
2	Aah14258	98.0	407	2	BAC85237	BAC85237 homo sapien
3	Aah14258	98.0	464	2	AAH1337	AAH1337 homo sapien
4	Aah14258	98.0	465	2	Q6GNX6	Q6GNX6 homo sapien
5	Aah14258	98.0	466	2	AAH4496	AAH4496 homo sapien
6	Aah14258	98.0	467	2	BAC81173	BAC81173 homo sapien
7	Aah14258	98.0	468	2	BAC81175	BAC81175 homo sapien
8	Aah14258	98.0	468	2	BAC8444	BAC8444 homo sapien
9	Aah14258	98.0	469	2	Q7ZP5	Q7ZP5 homo sapien
10	Aah14258	98.0	470	2	Q6PU44	Q6PU44 homo sapien
11	Aah14258	98.0	470	2	Q7Z5W1	Q7Z5W1 homo sapien
12	Aah14258	98.0	470	2	BAC85235	BAC85235 homo sapien
13	Aah14258	98.0	470	2	BAC85387	BAC85387 homo sapien
14	Aah14258	98.0	470	2	AAH63336	AAH63336 homo sapien
15	Aah14258	98.0	470	2	AAH14258	AAH14258 homo sapien
16	Aah14258	98.0	470	2	AAH1747	AAH1747 homo sapien
17	Aah14258	98.0	470	2	AAH2314	AAH2314 homo sapien
18	Aah14258	98.0	471	2	BAC83388	BAC83388 homo sapien
19	Aah14258	98.0	471	2	AAH2289	AAH2289 homo sapien
20	Aah14258	98.0	472	2	BAC8232	BAC8232 homo sapien
21	Aah14258	98.0	472	2	BAC8225	BAC8225 homo sapien
22	Aah14258	98.0	473	2	BAC0913	BAC0913 homo sapien
23	Aah14258	98.0	474	2	BAC85101	BAC85101 homo sapien
24	Aah14258	98.0	474	2	BAC05012	BAC05012 homo sapien
25	Aah14258	98.0	475	2	Q6GMW7	Q6GMW7 homo sapien
26	Aah14258	98.0	475	2	AAH26338	AAH26338 homo sapien
27	Aah14258	98.0	476	2	Q6GMX1	Q6GMX1 homo sapien
28	Aah14258	98.0	476	2	BAC05017	BAC05017 homo sapien
29	Aah14258	98.0	477	2	BAC83394	BAC83394 homo sapien
30	Aah14258	98.0	477	2	BAC85697	BAC85697 homo sapien
31	Aah14258	98.0	477	2	BAC05018	BAC05018 homo sapien

RESULT 1						
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AC	P01857;					
DT	21-JUL-1986	(Rel. 01, Created)				
DT	21-JUL-1986	(Rel. 01, Last sequence update)				
DT	01-OCT-2004	(Rel. 45, Last annotation update)				
DE	IG_Gamma-1_chain_C_region.					
GN	Name=IGHG1;					
OS	Homo_sapiens (Human)					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;					
NCBI_TaxID	9606;					
OX						
RN	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE-8224238; PubMed=6287432;					
RA	Cunningham B.A.; Rutishauser U.; Gall W.E.; Gottlieb P.D.,					
RA	Waxdal M.J.; Edelman G.M.;					
RA	"The covalent structure of a human Gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."					
RL	Biochemistry 9:3161-3170(1970).					
[1]						
RN	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).					
RP	SEQUENCE OF 136-329 (EU).					
RX	MEDLINE=71064025; PubMed=5530842;					
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H., Edelman G.M.;					
RA	"The covalent structure of a human gamma G-immunoglobulin. VIII. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."					
RT	Biochemistry 9:3171-3181(1970).					
[2]						
RN	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).					
RP	SEQUENCE (MYELOMA PROTEIN KOL). PMID=126475;					
RA	Ponstingl H., Hilschmann N.;					
RT	"The primary structure of a monoclonal IgG immunoglobulin (myeloma protein KOL). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure,"					
RT	Biochemistry 9:3171-3181(1970).					
[3]						
RN	SEQUENCE OF 136-329 (EU).					
RP	SEQUENCE OF THE COMPLETE STRUCTURE;					
RX	MEDLINE=71064025; PubMed=5530842;					
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H., Edelman G.M.;					
RA	"The covalent structure of a human gamma G-immunoglobulin. VIII. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."					
RT	Biochemistry 9:3171-3181(1970).					
[4]						
RN	SEQUENCE (MYELOMA PROTEIN NIE).					
RP	SEQUENCE (MYELOMA PROTEIN KOL). PMID=126475;					
RA	Ponstingl H., Hilschmann N.;					
RT	"The primary structure of a monoclonal IgG immunoglobulin (myeloma protein NIE). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure,"					
RT	Biochemistry 9:3171-3181(1970).					
[5]						
RN	SEQUENCE (MYELOMA PROTEIN KOL). PMID=63289131; PubMed=684944;					
RP	SEQUENCE (MYELOMA PROTEIN NIE). PMID=63289131; PubMed=684944;					
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;					
RT	"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."					
RT	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-164 (1976).					
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-164 (1976).					
[6]						
RN	SEQUENCE (MYELOMA PROTEIN NIE). PMID=63289131; PubMed=684944;					
RP	SEQUENCE (MYELOMA PROTEIN NIE). PMID=63289131; PubMed=684944;					
RA	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-164 (1976).					
RT	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-164 (1976).					
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-164 (1976).					
RN	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-164 (1976).					
RP	DISULFIDE BONDS.					
RA	DISULFIDE BONDS.					
RT	DISULFIDE BONDS.					
RP	DISULFIDE BONDS.					
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RT	DISULFIDE BONDS.					
RP	DISULFIDE BONDS.					
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Gall W.B., Edelman G.M.; "The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds"; *Biochemistry* 9:3188-3196(1970).

[7]

DISULFIDE BONDS
MEDLINE=7070267; PubMed=1002129;
Dreker L., Schwarz J., Reichel W., Hilschmann N.; "Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie), I: purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.," *Hoppe-Seyler's Z. Physiol. Chem.* 357:1515-1540(1976).
[8]

X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS)
MEDLINE=842208100; PubMed=7436608;

DOMAIN	111	223	CH2.
DOMAIN	224	330	CH3.
DISULFID	27	83	Interchain (with light chain).
DISULFID	103	103	Interchain (with heavy chain).
DISULFID	109	109	Interchain (with heavy chain).
DISULFID	112	112	Interchain (with heavy chain).
DISULFID	144	204	
DISULFID	250	308	N-linked (GlcNAc, -).
CARBONYL	180	180	K → R (in GIM(3) marker).
VARIANT	97	97	D → E (in \overline{GIM} (non-1) marker).
VARIANT	239	239	/FTId=VAR_003886.
VARIANT	241	241	/FTId=VAR_003887.
STRAND	23	24	L → M (in GIM(non-1) marker).
			/FTId=VAR_003888.

seniorfer J.;
 crystallographic refinement and atomic models of a human IgG fragment B of protein A from *Staphylococcus* aureus at 2.9- and 2.8-A resolution.¹¹
 MISCELLANEOUS: Nie has the GIM(17) aliootypic marker, 97-K, and the GIM(1) markers, 239-D and 241-L, KOI and EU sequences have the GIM(3) marker and the GIM (non-L) marker.
 MISCELLANEOUS: Nie also differs in the amidation states of 35, 116, 198, 269 and 272.
 MISCELLANEOUS: EU also differs in the amidation states of residues 155, 166, 177, 195, 198, 269, and 272, and in the order of residues 268-272.

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L; J00228; AAC82527.1; ALT_INIT.
; A33433; GHIIU.
; 1AJ7; X-ray; H=1-103.
; 1D5B; X-ray; B/H=1-101.
; 1D5I; X-ray; H=1-101.
; 1D6V; X-ray; H=1-101.
; 1DN2; X-ray; A/B=120-326.
; 1E4K; X-ray; A/B=1-329.
; 1FC1; X-ray; A/B=106-329.
; 1FC2; X-ray; D=106-329.
; 1FCC; X-ray; A=121-326.
; 1HZH; X-ray; H/K=1-330.
; 1ITZ; X-ray; B/D=1-103.
; 1IIS; X-ray; A/B=1-07-330.
; 1IIX; X-ray; A/B=1-07-330.
; 1L6X; X-ray; A=120-326.
; 1QQX; X-ray; A/B=119-330.
; 2RCS; X-ray; H=1-103.
ew; HGNC-1525; IGH1L.
ew; HGNC-1525; IGH1L.

CO:0001624; C:membrane fraction; NAS.
GO:0033823; F:antigen binding; TAS.
GO:0063655; P:immune response; NAS.
terPto; IPR007110; Ig-like.
m; PF00047; 19; 3.

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61	GLYLISSVTVPESSLGQTQIICNWNHKPSNTKVDKKEPRSDKTHTCPCKPAPBLLGG	120	Db	378 QCGNYFSCSYMHAEHNHYTQKSLSLSPGK 407
61	GLIQLSSVTVSSSLGTQIICNWNHKPSNTKVDKKEPRSDKTHTCPCKPAPBLLGG	120	RESULT 3	
121	PSYLFPPKPKDTLMISRTPEVTCVYDVSHEDEPEVKENWYDGEVHVKTPREEQYN	180	AAH19337	PRELIMINARY; PRT; 464 AA.
121	PSVLFPPKPKDTLMISRTPEVTCVYDVSHEDEPEVKENWYDGEVHVKTPREEQYN	180	AC	AAH19337; ID
121	PSVLFPPKPKDTLMISRTPEVTCVYDVSHEDEPEVKENWYDGEVHVKTPREEQYN	180	DI	02-MAR-2004 (TREMBLrel. 27, Created)
121	PSVLFPPKPKDTLMISRTPEVTCVYDVSHEDEPEVKENWYDGEVHVKTPREEQYN	180	DT	02-MAR-2004 (TREMBLrel. 27, Last sequence update)
181	STRYVSVLTVLHQNMNGKEYKCKVSKNKAQPIEKTISKAKVQPREPOVTLPPSRDE	240	DT	02-MAR-2004 (TREMBLrel. 27, Last annotation update)
181	STRYVSVLTVLHQDWLNGKEYKCKVSKNKAQPIEKTISKAKVQPREPOVTLPPSRDE	240	DE	Hypothetical protein.
181	STRYVSVLTVLHQDWLNGKEYKCKVSKNKAQPIEKTISKAKVQPREPOVTLPPSRDE	240	OS	Homo sapiens (Human).
181	STRYVSVLTVLHQDWLNGKEYKCKVSKNKAQPIEKTISKAKVQPREPOVTLPPSRDE	240	OC	Zukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
241	LTKNQVSLTCLVKPGFYSIDAVENSGOPENNYKTPPVLDGSFLYSLKLTVDKSRW	300	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
241	LTKNQVSLTCLVKPGFYSIDAVENSGOPENNYKTPPVLDGSFLYSLKLTVDKSRW	300	OX	NCBI_TaxID:9606;
241	LTKNQVSLTCLVKPGFYSIDAVENSGOPENNYKTPPVLDGSFLYSLKLTVDKSRW	300	RN	[1]
301	QQGNVFSCSYMHAEHNHYTQKSLSLSPGK 330	330	RP	SEQUENCE FROM N.A.
301	QQGNVFSCSYMHAEHNHYTQKSLSLSPGK 330	330	RC	TISSUE=Primary B-Cells;
301	QQGNVFSCSYMHAEHNHYTQKSLSLSPGK 330	330	RX	Medline=22388257; PubMed=12477932;
301	QQGNVFSCSYMHAEHNHYTQKSLSLSPGK 330	330	RA	Strausberg R.L., Feingold E.A., Grouse L.R., Degege J.G., Schuler G.D., Krausser R.D., Collins F.S., Wagner L., Shemesh C.M., Blat N.K., Altschul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Brat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Tohshiyuki S., Carninci P., Prange C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEvlan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fabey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boroffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimm J., Schmitz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailis D.E., Schnurch A., Schein J.E., Jones S.J., Marras M.A.; "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences"; RT and mouse cDNA sequences"; RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
301	QQGNVFSCSYMHAEHNHYTQKSLSLSPGK 330	330	RN [2]	SEQUENCE FROM N.A.
301	QQGNVFSCSYMHAEHNHYTQKSLSLSPGK 330	330	RP	TISSUE=Primary B-Cells;
301	QQGNVFSCSYMHAEHNHYTQKSLSLSPGK 330	330	RC	Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
301	QQGNVFSCSYMHAEHNHYTQKSLSLSPGK 330	330	RL	EMBL; BC019337; AAH19337.1; -.
301	QQGNVFSCSYMHAEHNHYTQKSLSLSPGK 330	330	DR	Hypothetical protein.
301	QQGNVFSCSYMHAEHNHYTQKSLSLSPGK 330	330	KW	SEQUENCE 464 AA; 50891 MW; 2F80673E74E2A485 CRC64;
301	QQGNVFSCSYMHAEHNHYTQKSLSLSPGK 330	330	SQ	Query Match Best local Similarity 97.9%; Pred. No. 1..3e-117; Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0; Score 1729; DB 2; Length 464;
301	QQGNVFSCSYMHAEHNHYTQKSLSLSPGK 330	330	Qy	1 ASTKGPSVFLPSSKSTGGTAALGCVYDVKDPEPTVSNNSGALTSGVHTFPVQLQSS 60
301	QQGNVFSCSYMHAEHNHYTQKSLSLSPGK 330	330	Db	78 ASTKGPSVFLPSSKSTGGTAALGCVYDVKDPEPTVSNNSGALTSGVHTFPVQLQSS 137
301	QQGNVFSCSYMHAEHNHYTQKSLSLSPGK 330	330	Qy	61 GLYLISSVTVPESSSLGTQIICNWNHKPSNTKVDKKEPRSDKTHTCPCKPAPBLLGG 120
301	QQGNVFSCSYMHAEHNHYTQKSLSLSPGK 330	330	Db	138 GLYLISSVTVPESSSLGTQIICNWNHKPSNTKVDKKEPRSDKTHTCPCKPAPBLLGG 197
301	QQGNVFSCSYMHAEHNHYTQKSLSLSPGK 330	330	Qy	121 PSVLFPPKPKDTLMISRTPEVTCVYDVSHEDEPEVKENWYDGEVHVKTPREEQYN 180
301	QQGNVFSCSYMHAEHNHYTQKSLSLSPGK 330	330	Db	198 PSVLFPPKPKDTLMISRTPEVTCVYDVSHEDEPEVKENWYDGEVHVKTPREEQYN 257
301	QQGNVFSCSYMHAEHNHYTQKSLSLSPGK 330	330	Qy	181 STRYVSVLTVLHQNMNGKEYKCKVSKNKAQPIEKTISKAKVQPREPOVTLPPSRDE 240
301	QQGNVFSCSYMHAEHNHYTQKSLSLSPGK 330	330	Db	258 STRYVSVLTVLHQDWLNGKEYKCKVSKNKAQPIEKTISKAKVQPREPOVTLPPSRDE 317
301	QQGNVFSCSYMHAEHNHYTQKSLSLSPGK 330	330	Qy	241 LTKNQVSLTCLVKPGFYSIDAVENSGOPENNYKTPPVLDGSFLYSLKLTVDKSRW 300
301	QQGNVFSCSYMHAEHNHYTQKSLSLSPGK 330	330	Db	318 LTKNQVSLTCLVKPGFYSIDAVENSGOPENNYKTPPVLDGSFLYSLKLTVDKSRW 377
301	QQGNVFSCSYMHAEHNHYTQKSLSLSPGK 330	330	Qy	375 LTKNQVSLTCLVKPGFYSIDAVENSGOPENNYKTPPVLDGSFLYSLKLTVDKSRW 434

				BAC85175	PRELIMINARY;	PRT;	468 AA.
)	121	PSVFLFPKPKDTLMISRTPVEVTCVVYDVSHEDPEVKENWYDGVEVHNYTKPREEQYN	180	ID BAC85175			
)	257	PSVFLFPKPKDTLMISRTPVEVTCVVYDVSHEDPEVKENWYDGVEVHNYTKPREEQYN	316	AC BAC85175;			
)	181	STYRVSVLTVLHQDWINGKEYCKVSKNALKAPIEKTISAKGQPREEQVTLPSSRDE	240	DT 02-MAR-2004 (TREMBrel. 27, Last sequence update)			
)	317	STYRVSVLTVLHQDWINGKEYCKVSKNALKAPIEKTISAKGQPREEQVTLPSSRDE	375	DT 02-MAR-2004 (TREMBrel. 27, Last annotation update)			
)	241	LTKQVSLTCLVKGPYPSDIAEVENGOPENNYKTPPVLDVSQFLYSKLTVDKSRW	300	DE CDNA FLJ26006 file, clone DMC08725, highly similar to Ig gamma-1 chain			
)	377	LTKQVSLTCLVKGPYPSDIAEVENGOPENNYKTPPVLDVSQFLYSKLTVDKSRW	436	DE C region.			
)	301	QQGNVFSCSVHEALHNHYQQRSLSPGK	330	OS Homo sapiens (Human).			
)	437	QQGNVFSCSVHEALHNHYTQKSLSPGK	466	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.			
)				OX NCBI_TaxID:9606;			
)				RN [1]			
)				RP SEQUENCE FROM N.A.			
)				RC TISSUE=Dermoid tumor;			
)				RA Ora T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama A., Sugiyama T., Irie R., Otuki T., Sato H., Nishikawa T., Sugiura S., Kawakami B., Nagai K., Isogai T., Sugano S., "NEDO human cDNA sequencing project.", Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.			
)				DR AKI1285175; BACB5175_1; -;			
)				SQ SEQUENCE 468 AA; 51266 MW; 11C519DB6AE3D44B CRC64;			
)				QY 1 ASTKGPRVPFAPSSKSSTSGGTAAAGCLVYKDPFEPPTVWSNNSGALTSGVHTFPAVLOSS 60			
)				DB 139 ASTKGPRVPFAPSSKSSTSGTAAGCLVYDPPFPTVWSNNSGALTSGVHTFPAVLOSS 198			
)				QY 61 GLYSLSVVTVPSSSLGQTYYICNVNHHKPSENTKYDKVKEPKSDKTHTCPCCPAPELIGG 120			
)				DB 199 GLYSLSVVTVPSSSLGQTYYICNVNHHKPSENTKYDKVKEPKSDKTHTCPCCPAPELIGG 258			
)				QY 121 PSVFLFPKPKTLMISRTPETVTCVYDVSHEDPEVKENWYDGVEVHNYTKPREEQYN 180			
)				DB 259 PSVFLFPKPKTLMISRTPETVTCVYDVSHEDPEVKENWYDGVEVHNYTKPREEQYN 318			
)				QY 181 STYRVSVLTVLHQDWINGKEYCKVSKNALKAPIEKTISAKVQPREQVTLPPSDE 240			
)				DB 319 STYRVSVLTVLHQDWINGKEYCKVSKNALKAPIEKTISAKVQPREQVTLPPSDE 378			
)				QY 241 LTQNOVSLTCLVKGPYPSDIAEVENGOPENNYKTPPVLDVSQFLYSKLTVDKSRW 300			
)				DB 379 LTQNOVSLTCLVKGPYPSDIAEVENGOPENNYKTPPVLDVSQFLYSKLTVDKSRW 438			
)				RESULT 8			
)				BAC85444 PRELIMINARY;			
)				ID BAC85444;			
)				AC BAC85444;			
)				DT 02-MAR-2004 (TREMBrel. 27, Last sequence update)			
)				DT 02-MAR-2004 (TREMBrel. 27, Last annotation update)			
)				DE C region.			
)				OS Homo sapiens (Human).			
)				OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.			
)				OX NCBI_TaxID:9606;			
)				RN [1]			
)				RP SEQUENCE FROM N.A.			
)				RC TISSUE=Rhymus;			
)				RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otuki T., Sato H., Nishikawa T., Nagai K., Isogai T., Sugano S.;			

RT	"NEDO human cDNA sequencing project.";	RA	Strausberg R.;
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.	RL	Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AKI0844; BAC8444.1; -	DR	EMBL; BC05138; AAH51328.1;
SEQUENCE	468 AA; 51224 MW; 9280ACAD6817FC20 CRC64;	DR	IntesPro; IPR07110; 19-like.
Query Match	98.0%: Score 1729; DE 2; Length 468;	DR	InterPro; IPR03597; Ig_C1.
Best Local Similarity	97.9%; Pred. No. 1 6e-117;	DR	InterPro; IPR03005; Ig_MHC.
Matches	323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;	DR	Pfam; PF01654; C1-set;
Qy	1 ASTKGPSVPLAPSSKSTSGGTAALGCLYDVFPEPTVWSNSGALTSGVHTFPVQLSS 60	DR	Pfam; SM00436; Ig_1.
Db	139 ASTKGPSVPLAPSSKSTSGGTAALGCLYDVFPEPTVWSNSGALTSGVHTFPVQLSS 198	DR	PROSITE; PS05035; Ig_MHC; UNKNOWN 2.
Qy	61 GLYSLSVVTVPSSTGQTYICNVNHPKSNTKVDKVBPKSCKDTHTCPCPAPELGG 120	SQ	PROSITE; PS05035; Ig_MHC; UNKNOWN 2.
Db	199 GLYSLSVVTVPSSTGQTYICNVNHPKSNTKVDKVBPKSCKDTHTCPCPAPELGG 258	Qy	51 ASTKGPSVPLAPSSKSTSGGTAALGCLYDVFPEPTVWSNSGALTSGVHTFPVQLSS 60
Qy	121 PSVFLPPPKPKDTLMISRPEVTCPVVDYSHDEBEVKENWYDGVEVINKTVPREEQYN 180	Qy	52 ASTKGPSVPLAPSSKSTSGGTAALGCLYDVFPEPTVWSNSGALTSGVHTFPVQLSS 199
Db	259 PSVFLPPPKPKDTLMISRPEVTCPVVDYSHDEBEVKENWYDGVEVINKTVPREEQYN 318	Db	98.0%: Score 1729; DB 2; Length 469;
Qy	181 STYRVISVLTVLHQDLNGKEYKCVSNKALPAPTEKTIKSKAVQPREPVYTLPQRSDR 240	Best Local Similarity 97.9%; Pred. No. 1 6e-117;	Best Local Similarity 97.9%; Pred. No. 1 6e-117;
Db	319 STYRVISVLTVLHQDLNGKEYKCVSNKALPAPTEKTIKSKAVQPREPVYTLPQRSDR 378	Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;	Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy	241 LTKNOVSLLTCLVKGPFPSDIAVEWRSNGOPENNYKTPPEVLDVGFFLYSKLTVDKSRW 300	Qy	61 GLYSLSVVTVPSSTGQTYICNVNHPKSNTKVDKVBPKSCKDTHTCPCPAPELGG 120
Db	379 LTKNOVSLLTCLVKGPFPSDIAVEWRSNGOPENNYKTPPEVLDVGFFLYSKLTVDKSRW 438	Db	200 GLYSLSVVTVPSSTGQTYICNVNHPKSNTKVDKVBPKSCKDTHTCPCPAPELGG 120
Qy	301 QOGNVFSCSYNHEA1INHYQORSLSLSPGK 330	Qy	121 PSVFLPPPKPKDTLMISRPEVTCPVVDYSHDEBEVKENWYDGVEVINKTVPREEQYN 180
Db	439 QOGNVFSCSYNHEA1INHYQORSLSLSPGK 468	Db	260 PSVFLPPPKPKDTLMISRPEVTCPVVDYSHDEBEVKENWYDGVEVINKTVPREEQYN 319
RESULT 9			
ID	Q7Z7P5	PRELIMINARY;	469 AA.
AC	Q7Z7P5;	PRT;	469 AA.
DT	01-OCT-2003 (TREMBLrel. 25; Created)	Qy	121 PSVFLPPPKPKDTLMISRPEVTCPVVDYSHDEBEVKENWYDGVEVINKTVPREEQYN 180
DT	01-OCT-2003 (TREMBLrel. 25; Last sequence update)	Db	241 LTKNOVSLLTCLVKGPFPSDIAVEWRSNGOPENNYKTPPEVLDVGFFLYSKLTVDKSRW 300
DT	01-MAR-2004 (TREMBLrel. 26; Last annotation update)	Qy	241 LTKNOVSLLTCLVKGPFPSDIAVEWRSNGOPENNYKTPPEVLDVGFFLYSKLTVDKSRW 300
DE	IGHG1 protein.	Db	380 LTKNOVSLLTCLVKGPFPSDIAVEWRSNGOPENNYKTPPEVLDVGFFLYSKLTVDKSRW 438
OS	Homo sapiens (Human)	Qy	301 QOGNVFSCSYNHEA1INHYQORSLSLSPGK 330
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi;	Qy	301 QOGNVFSCSYNHEA1INHYQORSLSLSPGK 468
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Db	440 QOGNVFSCSYNHEA1INHYQORSLSLSPGK 469
RN	[1] _TaxID=9606;	RESULT 10	
RP	SEQUENCE FROM N.A.	Q6PJA4	PRELIMINARY;
RC	TISSUE=Spleen.	Q6PJA4	PRT;
RA	MEDLINE=22388237; PubMed=12477932;	Q6PJA4;	470 AA.
RA	Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G., Schuler G.D., TISSUE=Primary B-Cells;	Q6PJA4;	
RA	Klaunser R.D., Collins F.S., Wagner L., Shanmam C.M., Schuler G.D., TISSUE=	DT	05-JUL-2004 (TREMBLrel. 27; Created)
RA	Richards S., Mcowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., TISSUE=	DT	05-JUL-2004 (TREMBLrel. 27; Last annotation update)
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Homo sapiens (Human)	DE	Hypothetical protein.
RA	Hopkins R.P., Jordan A., Moore T., Max S.I., Wang J., Hsieh P., Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi;	OS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., NCBI TaxID=9606;	OX	NCBI TaxID=9606;
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RN	RN	SEQUENCE FROM N.A.
RA	Brownstein M.B., Usdin T.B., Toshiyuki S., Carninci P., Prange C., TISSUE=	RC	TISSUE=
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., B-Cells;	RC	B-Cells;
RA	Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G., Schuler G.D., TISSUE=	RX	Medline=22388237; PubMed=12477932;
RA	Klaunser R.D., Collins F.S., Wagner L., Shanmam C.M., Schuler G.D., TISSUE=	RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., TISSUE=
RA	Richards S., Mcowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., TISSUE=	RA	Auerschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Bhat N.K., TISSUE=
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., TISSUE=	RA	Dietcheiko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., TISSUE=
RA	Hopkins R.P., Jordan A., Moore T., Max S.I., Wang J., Hsieh P., TISSUE=	RA	Stipletton M., Scores M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., TISSUE=
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., TISSUE=	RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., TISSUE=
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., TISSUE=	RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., TISSUE=
RA	Brownstein M.B., Usdin T.B., Toshiyuki S., Carninci P., Prange C., TISSUE=	RA	Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Garnierine P.H., TISSUE=
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., TISSUE=	RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., TISSUE=
RA	Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G., Schuler G.D., TISSUE=	RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., TISSUE=
RA	Klaunser R.D., Collins F.S., Wagner L., Shanmam C.M., Schuler G.D., TISSUE=	RA	Fahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., TISSUE=
RA	Richards S., Mcowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., TISSUE=	RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Boutefeld G.G., TISSUE=
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., TISSUE=	RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., TISSUE=
RA	Hopkins R.P., Jordan A., Moore T., Max S.I., Wang J., Hsieh P., TISSUE=	RA	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., TISSUE=	RA	
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RA	Hopkins R.P., Jordan A., Moore T.,		

Rodriguez A.C., Grimmwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krywinski M.I., Skalska J., Smailius D.E., Schein J.E., Jones S.J., Marrs M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

SEQUENCE FROM N.A.

TISSUE=Primary B-Cells;

Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

EMBL: BC018747; AAH18747.1; -.

InterPro: IPRO03599; Ig-like.

InterPro: IPRO07110; Ig-like.

InterPro: IPRO03597; Ig^{cl}.

InterPro: IPRO03006; Ig^{MHC}.

InterPro: IPRO03516; Ig^v.

Pfam: PF007634; Cl-set;

PFAM: PF00047; Ig⁴.

SMART: SM00409; Ig⁴.

SMART: SM00407; IgC1; 3.

SMART: SM00406; IgV; 1.

PROSITE: PS51835; Ig-LIKE; 4.

PROSITE: PS00290; Ig_MHC; UNKNOWN_2.

Hypothetical protein; SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 98.0%; Score 1729; DB 2; Length 470; Best Local Similarity 97.9%; Pred. No. 1..6-117; Indels 0; Gaps 0; Matches 323; Conservative 3; Mismatches 0; Gaps 0;

1 ASTKGPSVPEPLAPS SKSTSGGTAALGCLVKDYFPEPYTVSKNSGALTSGVHTFPAPVQSS 60

141 ASTKGPSVPEPLAPS SKSTSGGTAALGCLVKDYFPEPYTVSKNSGALTSGVHTFPAPVQSS 200

61 GLISLSSVTVPSLSSIGLTQTYCNVNPKSNKVDKKEPKSCDKTHTCPCPAPELGG 120

201 GLYLSISSVTVPSLSSIGLTQTYCNVNPKSNKVDKKEPKSCDKTHTCPCPAPELGG 260

121 PSVLFPPKPKDTMISMISRTPEVTVVVVDPEVKNWYDGEVHNAXTKPPEEQN 180

141 PSVLFPPKPKDTMISMISRTPEVTVVVVDPEVKNWYDGEVHNAXTKPPEEQN 320

261 PSVLFPPKPKDTMISMISRTPEVTVVVVDPEVKNWYDGEVHNAXTKPPEEQN 320

181 STYRVVSVLTVLHQDWKNGKEYKCKVSNKALPAPIEKTISKAKVOREPQQYTLPSRDE 240

321 STYRVVSVLTVLHQDWKNGKEYKCKVSNKALPAPIEKTISKAKGQRREPQQYTLPSRDE 380

241 LTKRQVSLTCLVKGYFPSDIAVEWESNGOPENNYKTRTPPVLDGSVGSFFLYSKLTVDKSRW 300

381 LTKRQVSLTCLVKGYFPSDIAVEWESNGOPENNYKTRTPPVLDGSFPLYSKLTVDKSRW 440

301 QGNNYFSCSYMEHALHNHYTQRSLSLRGK 330

441 QGNNYFSCSYMEHALHNHYTQKSLSLRGK 470

RESULT 11

Q7Z5W1 PRELIMINARY; PRT; 470 AA.

Q7Z5W1 PRELIMINARY; PRT; 470 AA.

01-OCT-2003 (TRIMBrel. 25, Created)

01-OCT-2003 (TRIMBrel. 25, Last sequence update)

01-MAR-2004 (TRIMBrel. 26, Last annotation update)

Hypothetical protein.

Homo sapiens (Human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo; NCBI_TaxID:9606;

[1] PRELIMINARY; PRT; 470 AA.

SEQUENCE FROM N.A.

TISSUE=Spleen

MEDLINE=2138857; PubMed=12477932;

Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.,

Klauser R.D., Collins F.S., Wagner L., Shanmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Ronald M.P., Casavant T.L., Scheetz T.B., Stapleton M., Soares M.B., Farmer A.A., Rubin G.M., Hong L., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Baha S.S., Loquai N.A., Peters G.J., Abramson D.D., Mullaly S.J., Bosak S.A., McElwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulick S.W., Villalon D.K., Muniz D.M., Sodergren E.J., Lu X., Gibbs R.A., Rehey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailius D.E., Schnurch A., Schein J.E., Jones S.J., Marrs M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RT [2].

RN RN

SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RC Strusberg R.; Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

RL EMBL: BC051984; AAH3984.1; -.

DR InterPro: IPR007110; Ig-Like.

DR InterPro: IPR003597; Ig_L1.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003596; Ig_V.

DR Pflam; PFO0754; Cl-set; 3.

DR Pflam; PFO0047; Ig_1.

DR SMART: SM00406; IgV; 1.

DR PROSITE; PS50835; Ig_LIKE; 4.

DR PROSITE; PS00290; Ig_MHC; UNKNOWN_2.

KW Hypothetical protein.

SEQUENCE 470 AA; 51204 MW; 770CF34521483ELA CRC64;

Query Match 98.0%; Score 1729; DB 2; Length 470; Best Local Similarity 97.9%; Pred. No. 1..6-117; Indels 0; Gaps 0; Matches 323; Conservative 3; Mismatches 4; Gaps 0;

QY 1 ASTKGPSVPEPLAPS SKSTSGGTAALGCLVKDYFPEPYTVSKNSGALTSGVHTFPAPVLOSS 60

Db 141 ASTKGPSVPEPLAPS SKSTSGGTAALGCLVKDYFPEPYTVSKNSGALTSGVHTFPAPVLOSS 200

QY 1 ASTKGPSVPEPLAPS SKSTSGGTAALGCLVKDYFPEPYTVSKNSGALTSGVHTFPAPVLOSS 60

Db 141 ASTKGPSVPEPLAPS SKSTSGGTAALGCLVKDYFPEPYTVSKNSGALTSGVHTFPAPVLOSS 200

QY 61 GLYLSISSVTVPSLSSIGLTQTYCNVNPKSNKVDKKEPKSCDKTHTCPCPAPELGG 120

Db 201 GLYLSISSVTVPSLSSIGLTQTYCNVNPKSNKVDKKEPKSCDKTHTCPCPAPELGG 260

QY 121 PSVLFPPKPKDTMISMISRTPEVTVVVVDPEVKNWYDGEVHNAXTKPPEEQN 180

Db 141 PSVLFPPKPKDTMISMISRTPEVTVVVVDPEVKNWYDGEVHNAXTKPPEEQN 320

QY 261 PSVLFPPKPKDTMISMISRTPEVTVVVVDPEVKNWYDGEVHNAXTKPPEEQN 320

Db 181 STYRVVSVLTVLHQDWKNGKEYKCKVSNKALPAPIEKTISKAKVOREPQQYTLPSRDE 240

Db 321 STYRVVSVLTVLHQDWKNGKEYKCKVSNKALPAPIEKTISKAKGQRREPQQYTLPSRDE 380

QY 241 LTKRQVSLTCLVKGYFPSDIAVEWESNGOPENNYKTRTPPVLDGSVGSFFLYSKLTVDKSRW 300

Db 381 LTKRQVSLTCLVKGYFPSDIAVEWESNGOPENNYKTRTPPVLDGSFPLYSKLTVDKSRW 440

QY 301 QGNNYFSCSYMEHALHNHYTQRSLSLRGK 330

Db 441 QGNNYFSCSYMEHALHNHYTQKSLSLRGK 470

QY 181 STYRVVSVLTVLHQDWKNGKEYKCKVSNKALPAPIEKTISKAKVOREPQQYTLPSRDE 240

Db 321 STYRVVSVLTVLHQDWKNGKEYKCKVSNKALPAPIEKTISKAKVOREPQQYTLPSRDE 380

QY 241 LTKRQVSLTCLVKGYFPSDIAVEWESNGOPENNYKTRTPPVLDGSFPLYSKLTVDKSRW 300

Db 381 LTKRQVSLTCLVKGYFPSDIAVEWESNGOPENNYKTRTPPVLDGSFPLYSKLTVDKSRW 440

QY 301 QGNNYFSCSYMEHALHNHYTQRSLSLRGK 330

Db 441 QGNNYFSCSYMEHALHNHYTQKSLSLRGK 470

•RESULT 12

BAC55235 PRELIMINARY; PRT; 470 AA.

ID BAC55235

AC BAC55235;

SEQID 1

DT 02-MAR-2004 (TRIMBrel. 27, Created)

DT 02-MAR-2004 (TRIMBrel. 27, Last sequence update)

DT 02-MAR-2004 (TRIMBrel. 27, Last annotation update)

DT 02-MAR-2004 (TRIMBrel. 27, Last annotation update)

DE	CDDNA FLJ26276 Fis, clone DMC06522, highly similar to Ig gamma-1 chain C region.	Query Match Score 98.0%; Best Local Similarity 97.9%; Matches 323; Conservative Matches 323; Mismatches 3; Indels 0; Gaps 0;
OS	Homo sapiens (Human)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
NCBII_TaxID	9606;	
RN	[1] -	
RP	SEQUENCE FROM N.A.	
RC	TISSUE-Dermoid tumor;	
RA	Ora T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y., Hata H., Nakagawa K., Miunuki S., Morinaga M., Kawamura M., SugiYama T., Irie R., Otsubo T., Sato H., Nishikawa T., Sugiyama A., Sugiyama T., Nagai K., Isogai T., Sugano S.; "NEDO human cDNA sequencing project"; Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.	
RA	"NEDO human cDNA sequencing project"; Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.	
DR	EMBL: AK129787; BAC95235; 1; -	
SQ	SEQUENCE 470 AA; 51090 MW; 460F471D4528A16 CRC64;	
Query Match Score 98.0%; Best Local Similarity 97.9%; Matches 323; Conservative Matches 323; Mismatches 3; Indels 0; Gaps 0;		
Db	1 ASTKGPSVPLAPSSKSTSGTAAIGCLVYDKYDFPEPVTVSNNGALTSGVHTFPVQSS 60	QY 121 PSVFLPPKPKDTMISRTPEVTCVVDYDSEDPEVKPSNTKVDKVEPKSKCDSKTHCPCPAPBLLGG 120
Db	141 ASTKGGSVPLAPSSKSTSGTAAIGCLVYDKYDFPEPVTVSNNGALTSGVHTFPVQSS 200	QY 141 ASTKGPSVPLAPSSKSTSGTAAIGCLVYDKYDFPEPVTVSNNGALTSGVHTFPVQSS 200
Qy	61 GLYLSVVTVTLPSSSLGTQTYICNNHKSNTKVDKVEPKSKCDSKTHCPCPAPBLLGG 180	QY 61 GLYLSVVTVTLPSSSLGTQTYICNNHKSNTKVDKVEPKSKCDSKTHCPCPAPBLLGG 180
Db	201 GLYLSVVTVTLPSSSLGTQTYICNNHKSNTKVDKVEPKSKCDSKTHCPCPAPBLLGG 260	QY 201 GLYLSVVTVTLPSSSLGTQTYICNNHKSNTKVDKVEPKSKCDSKTHCPCPAPBLLGG 260
Qy	181 STYRVSVLTVLHQNWANGKEYKCKVSNKALPATEKTIKAKVQREPQVTILPSPRDE 240	QY 181 STYRVSVLTVLHQNWANGKEYKCKVSNKALPATEKTIKAKVQREPQVTILPSPRDE 240
Db	321 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPATEKTIKAKVQREPQVTILPSPRDE 380	QY 321 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPATEKTIKAKVQREPQVTILPSPRDE 380
Qy	321 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPATEKTIKAKVQREPQVTILPSPRDE 380	QY 321 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPATEKTIKAKVQREPQVTILPSPRDE 380
Db	381 LTKNOVSLTCLVKGFYPSDAVEWESNGOPENNYKTTPVLDVGSSFFLYSKLTVDKSRW 300	QY 381 LTKNOVSLTCLVKGFYPSDAVEWESNGOPENNYKTTPVLDVGSSFFLYSKLTVDKSRW 300
Qy	381 LTKNOVSLTCLVKGFYPSDAVEWESNGOPENNYKTTPVLDVGSSFFLYSKLTVDKSRW 440	QY 381 LTKNOVSLTCLVKGFYPSDAVEWESNGOPENNYKTTPVLDVGSSFFLYSKLTVDKSRW 440
Db	301 QGNVFSCSVVMHEALTHNHYCQRSLSLSPGK 330	QY 301 QGNVFSCSVVMHEALTHNHYCQRSLSLSPGK 330
Qy	441 QGNVFSCSVVMHEALTHNHYCQRSLSLSPGK 470	QY 441 QGNVFSCSVVMHEALTHNHYCQRSLSLSPGK 470
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Spleen;	
	MEDLINE=2388257; Pubmed=12477932;	
RX	Strausberg R.L., Grouse L.H., Derge J.G., AC AAH62336; PRELIMINARY; PRT: 470 AA.	
RA	Klaushner R.D., Collins P.S., Wagner L., Schuler G.D., AC AAH62336; PRELIMINARY; PRT: 470 AA.	
RA	Altatchul S.F., Zeeberg B.R., Buetow K.B., Scheuer C.P., Bhat N.K., Hsieh F., AC AAH62336; PRELIMINARY; PRT: 470 AA.	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Prange C., Brownstein M.J., Usdin T.B., Toshiyuki S., Garnicini P., Bhat N.K., Hsieh F., AC AAH62336; PRELIMINARY; PRT: 470 AA.	
RA	Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., AC AAH62336; PRELIMINARY; PRT: 470 AA.	
RA	Stepleton M.J., Brownstein M.J., Zeeberg B.R., Wagner L., Schuler G.D., Buetow K.B., Scheuer C.P., Bhat N.K., Hsieh F., AC AAH62336; PRELIMINARY; PRT: 470 AA.	
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Garnicini P., Prange C., Brownstein M.J., Zeeberg B.R., Wagner L., Schuler G.D., Buetow K.B., Scheuer C.P., Bhat N.K., Hsieh F., AC AAH62336; PRELIMINARY; PRT: 470 AA.	
RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahay S.J., Boak S.A., McEvans P.J.J., McKernan K.J.J., Malek J.A., Richards S., Worley K.C., Garcia A.M., Gay L.J., Hulyk S.W., AC AAH62336; PRELIMINARY; PRT: 470 AA.	
RA	Fahy J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krywinski M.I., Skalska U., Smaitis D.E., Schneich A., Schein J.E., Jones S.J., Marra M.A., AC AAH62336; PRELIMINARY; PRT: 470 AA.	
RA	"Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	
RT	RT and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	
RN	[2] STRAUSBERG R.L.; Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.	
RP	SEQUENCE FROM N.A.	
RC	Kanehori K., Ishibashi T., Chiba Y., Fujimori K., HiraoKA S., Watanabe S., Ishida S., Ono Y., Mizuno S., Morinaga M., Kawamura M., Suzuki Y., Hata H., Watanabe S., Itoh T., Watanabe M., Sugiyama T., Sugiyama T., Irie R., Orsuki T., Sato H., Nishikawa T., Sugiyama S.; "NEDO human cDNA sequencing project"; Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.	
RA	"NEDO human cDNA sequencing project"; Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.	
DR	EMBL: AK130585; BAC95387; 1; -	
SQ	SEQUENCE 470 AA; 51642 MW; D8C43B61A782293C CRC64;	

Query Match 98.0%; Score 1729; DB 2; Length 470;
 Best Local Similarity 97.9%; Pred. No. 1.6e-117;
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1	ASTKGPSVFPLAISKTSKGTAAAGLGLVDRYFPEPVTVWNSGALTSGVHTFPVLOSS	60	Qy	1	ASTKGPSVFPLAISKTSKGTAAAGLGLVDRYFPEPVTVWNSGALTSGVHTFPVLOSS	60
141	ASTKGPSVFPLAISKTSKGTAAAGLGLVDRYFPEPVTVWNSGALTSGVHTFPVLOSS	200	Db	141	ASTKGPSVFPLAISKTSKGTAAAGLGLVDRYFPEPVTVWNSGALTSGVHTFPVLOSS	200
61	GLYSLSSTVTPSSLSGQTQYICNNHHKPSTKVKDKEKVEPKSCDTHTCPCPAPELIGG	120	Qy	61	GLYSLSSTVTPSSLSGQTQYICNNHHKPSTKVKDKEKVEPKSCDTHTCPCPAPELIGG	120
201	GLYSLSSTVTPSSLSGQTQYICNNHHKPSTKVKDKEKVEPKSCDTHTCPCPAPELIGG	260	Db	201	GLYSLSSTVTPSSLSGQTQYICNNHHKPSTKVKDKEKVEPKSCDTHTCPCPAPELIGG	260
121	PSVFLPPKPKDLMISRTEVTCVVDVSHEDEVKENMYDGYEVINVKTKPREEQYN	180	Qy	121	PSVFLPPKPKDLMISRTEVTCVVDVSHEDEVKENMYDGYEVINVKTKPREEQYN	180
261	PSVFLPPKPKDLMISRTEVTCVVDVSHEDEVKENMYDGYEVINVKTKPREEQYN	320	Db	261	PSVFLPPKPKDLMISRTEVTCVVDVSHEDEVKENMYDGYEVINVKTKPREEQYN	320
181	STYRVVSLLTIVLHQNWNGKEYKCKVSNTALPAPIEKTISKAVQPREPOVTLPPSRDE	240	Qy	181	STYRVVSLLTIVLHQNWNGKEYKCKVSNTALPAPIEKTISKAVQPREPOVTLPPSRDE	240
321	STYRVVSLLTIVLHQDLNGKEYKCKVSNTALPAPIEKTISKAVQPREPOVTLPPSRDE	380	Db	321	STYRVVSLLTIVLHQDLNGKEYKCKVSNTALPAPIEKTISKAVQPREPOVTLPPSRDE	380
241	LTKNQSLTLCVGFYPSDIAVEWNSNGOPENNYKTPVLDGSFFLYSKLTVDKSRW	300	Qy	241	LTKNQSLTLCVGFYPSDIAVEWNSNGOPENNYKTPVLDGSFFLYSKLTVDKSRW	300
381	LTKNQSLTLCVGFYPSDIAVEWNSNGOPENNYKTPVLDGSFFLYSKLTVDKSRW	440	Db	381	LTKNQSLTLCVGFYPSDIAVEWNSNGOPENNYKTPVLDGSFFLYSKLTVDKSRW	440
301	QQGNVPSCSVMHEALTHNHYQORSLSLSPGK	330	Qy	301	QQGNVPSCSVMHEALTHNHYQORSLSLSPGK	330
441	QQGNVPSCSVMHEALTHNHYQORSLSLSPGK	470	Db	441	QQGNVPSCSVMHEALTHNHYQORSLSLSPGK	470

JRESULT 15
 H14258 PRELIMINARY; PRT; 470 AA.
 AAH14258; Created)
 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
 Hypothetical protein.
 Homo sapiens (Human).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI TaxID=9606;
 [1] -

SEQUENCE FROM N.A.
 TISSUE=P-Primary B-cells
 MEDLINE=1238257; PubMed=12477912;
 Klausner R.D., Peingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 Altenschul S.F., Zeeberg B., Buetow K.H., Wagner L., Shenmen C.M., Bhat N.K.,
 Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Logueillo N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 Bosak S.A., McErlean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahay J., Heilman E., Keitman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Krzywinski M.I., Skalska U., Smallius D.E., Schnurch A., Schein J.E.,
 Jones S.J., Marrs M.A.; "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [2] -
 SEQUENCE FROM N.A.
 TISSUE=Primary B-Cells;
 Strausberg R.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 EMBL: BC014258; AAH14258.1;
 Hypothetical protein.

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CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic dermatitis, severe food allergies, chronic urticaria, angioedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, type-I diabetes mellitus, or multiple sclerosis, and for preventing of, or symptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present sequence is the human IgG1 heavy chain constant region

XX Sequence 330 AA;

```
Query Match 100.0%; score 1764; DB 6; Length 330;
Best Local Similarity 100.0%; Pred No 3 8e-125;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 ASTKGPSVFPKAPSSKSTSGGTAALGCLVKDYFPEPVTYWSNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPKAPSSKSTSGGTAALGCLVKDYFPEPVTYWSNSGALTSGVHTFPAVLQSS 60
Qy 61 GLYSSLSSVTVSSSISGQTQTCVNNHKPSNTKVDKVEPKSCDKTHICCPCPAPELIGG 120
Db 61 GLYSSLSSVTVSSSISGQTQTCVNNHKPSNTKVDKVEPKSCDKTHICCPCPAPELIGG 120
Qy 121 PSYFLPPKPKDILMSRTPEVTCVYDVSHEDPVKFWYDGVETWVKTPREOYN 180
Db 121 PSYFLPPKPKDILMSRTPEVTCVYDVSHEDPVKFWYDGVETWVKTPREOYN 180
Qy 181 STYRVSVLTVLHQINNGKEYKCKVSNKALPAPTEKTIASKVQPREPQVTLPPSRDE 240
Db 181 STYRVSVLTVLHQINNGKEYKCKVSNKALPAPTEKTIASKVQPREPQVTLPPSRDE 240
Qy 241 LTENQVSITLCLVKRGPFDIASEWENGOPENNYYKTPPVLDVGFFLYSKLTVDGSRW 300
Db 241 LTENQVSITLCLVKRGPFDIASEWENGOPENNYYKTPPVLDVGFFLYSKLTVDGSRW 300
Qy 301 QQQNFPSCSVMHEALHYHQORSLISLSPGK 330
Db 301 QQQNFPSCSVMHEALHYHQORSLISLSPGK 330
```

RESULT 2
ID AAB04071 standard; protein; 330 AA.
AC AAB04071;
XX DT 11-APR-2001 (first entry)

XX Zcytor 10: IgG gamma fusion peptide.
DE

XX zcytor 10 cytokine receptor; cytokine; receptor; antibody; ligand; binding; detection; modulation; recombinant cell; haemopoietic cell; lymphoid cell; myeloid cell; lymph; immune system; blood; bone; inflammatory response; inflammation; spleen; human.

OS Synthetic.
 OS Homo sapiens.
 XX PN WO200068381-A1.

XX PD 16-NOV-2000.
 XX PF 11-MAY-2000; 2000WO-US01924.
 .XX PR 11-MAY-1999;
 XX (ZYMO) ZYMOGENETICS INC.

XX PI Presnell SR, Foster DC, Hammond AK, Lok S;
 XX DR WPI: 2001-016036/02.
 DR N-PSDB; AAA54473.
 XX PT New cytokine receptor mouse zcytor 10, useful for detecting ligands that

stimulate proliferation or development of hematopoietic, lymphoid and myeloid cells.

XX Example 17; Page 120-121; 134pp; English.

XX Isolating a nucleotide which encodes the zcytor 10 cytokine receptor enables the production of recombinant cells expressing the receptor. Those cells can then be used to detect the presence of a modulator of zcytor 10 protein by culturing the cells in the presence and absence of the test sample. Similarly, detection of zcytor 10 receptor ligand within a test sample can be achieved. The method comprising contacting a test sample containing an amino acid sequence from Cys15 or Gly25 to Pro230 to Pro230 of the zcytor 10 cytokine receptor and detecting the binding of the polypeptide to a ligand in the sample. Specified peptide fragments of the zcytor 10 cytokine receptor and the methods described are used to identify ligands that stimulate the proliferation and/or development of hematopoietic, lymphoid and myeloid cells. Peptide fragments of the cytokine receptor are useful for treating lymphoid, immune, inflammatory, splenic, blood or bone disorders and for generating antibodies directed against the receptor. A vector expressing a secreted human zcytor 10 heterodimer is constructed. In this construct the extracellular cytokine binding domain of zcytor 10 is fused to the heavy chain of IgG Gamma and the extracellular portion of the heteromeric cytokine receptor subunit (an interleukin receptor subunit) is fused to human kappa light chain (See GENSEQ record AAA54474). The two sequences are fused together using two primers (AAA54475, AAA54476).

XX SQ Sequence 330 AA;

```
Query Match 98.0%; Score 1729; DB 4; Length 330;
Best Local Similarity 97.9%; Pred. No. 1.7e-122;
Matches 322; Conservative 3; Mismatches 14; Indels 0; Gaps 0;
Db 1 ASTKGPSVPLAPS SKSTS SGGTAA ALGCL VKYD PEP VTYS NSGALT SGVH TFP AVLQSS 60
Db 1 ASTKGPSVPLAPS SKSTS SGGTAA ALGCL VKYD PEP VTYS NSGALT SGVH TFP AVLQSS 60
Qy 61 GLYSSLSSVTVSSSISGQTQTCVNNHKPSNTKVDKVEPKSCDKTHICCPCPAPELIGG 120
Db 61 GLYSSLSSVTVSSSISGQTQTCVNNHKPSNTKVDKVEPKSCDKTHICCPCPAPELIGG 120
Qy 121 PSYFLPPKPKDILMSRTPEVTCVYDVSHEDPVKFWYDGVETWVKTPREOYN 180
Db 121 PSYFLPPKPKDILMSRTPEVTCVYDVSHEDPVKFWYDGVETWVKTPREOYN 180
Qy 181 STYRVSVLTVLHQINNGKEYKCKVSNKALPAPTEKTIASKVQPREPQVTLPPSRDE 240
Db 181 STYRVSVLTVLHQINNGKEYKCKVSNKALPAPTEKTIASKVQPREPQVTLPPSRDE 240
Qy 241 LTENQVSITLCLVKRGPFDIASEWENGOPENNYYKTPPVLDVGFFLYSKLTVDGSRW 300
Db 241 LTENQVSITLCLVKRGPFDIASEWENGOPENNYYKTPPVLDVGFFLYSKLTVDGSRW 300
Qy 301 QQQNFPSCSVMHEALHYHQORSLISLSPGK 330
Db 301 QQQNFPSCSVMHEALHYHQORSLISLSPGK 330
```

```
Query Match 98.0%; Score 1729; DB 4; Length 330;
Best Local Similarity 97.9%; Pred. No. 1.7e-122;
Matches 322; Conservative 3; Mismatches 14; Indels 0; Gaps 0;
Db 1 ASTKGPSVPLAPS SKSTS SGGTAA ALGCL VKYD PEP VTYS NSGALT SGVH TFP AVLQSS 60
Db 1 ASTKGPSVPLAPS SKSTS SGGTAA ALGCL VKYD PEP VTYS NSGALT SGVH TFP AVLQSS 60
Qy 61 GLYSSLSSVTVSSSISGQTQTCVNNHKPSNTKVDKVEPKSCDKTHICCPCPAPELIGG 120
Db 61 GLYSSLSSVTVSSSISGQTQTCVNNHKPSNTKVDKVEPKSCDKTHICCPCPAPELIGG 120
Qy 121 PSVFLPPKPKDILMSRTPEVTCVYDVSHEDPVKFWYDGVETWVKTPREOYN 180
Db 121 PSVFLPPKPKDILMSRTPEVTCVYDVSHEDPVKFWYDGVETWVKTPREOYN 180
Qy 181 STYRVSVLTVLHQINNGKEYKCKVSNKALPAPTEKTIASKVQPREPQVTLPPSRDE 240
Db 181 STYRVSVLTVLHQINNGKEYKCKVSNKALPAPTEKTIASKVQPREPQVTLPPSRDE 240
Qy 241 LTENQVSITLCLVKRGPFDIASEWENGOPENNYYKTPPVLDVGFFLYSKLTVDGSRW 300
Db 241 LTENQVSITLCLVKRGPFDIASEWENGOPENNYYKTPPVLDVGFFLYSKLTVDGSRW 300
Qy 301 QQQNFPSCSVMHEALHYHQORSLISLSPGK 330
Db 301 QQQNFPSCSVMHEALHYHQORSLISLSPGK 330
```

RESULT 3
ID AAA47856 standard; protein; 330 AA.
XX AC AAA47856;
XX DT 22-FEB-2002 (first entry)
XX DE Human Ig-gamma heavy chain constant region amino acid sequence.
XX KW Human; immunoadhesin; intercellular adhesion molecule ICAM-1;
KW human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold;
KW transgenic plant.
XX

CC recuperation from chemotherapy, recuperation from irradiation therapy, or
 CC a condition or symptom related to the above mentioned diseases in a
 CC mammal. The present sequence is human DR6 protein-related protein
 XX Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 5; Length 330;
 Best Local Similarity 97.9%; Pred. No. 1.7e-122;
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 SQ **ASTKGPSVPLAPSSKSTSGGTAALCCLVVDYFPBPVTVWSNSGALTSGVHHTFPAVIQQS** 60
Db 1 ASTKGPSVPLAPSSKSTSGGTAALCCLVVDYFPBPVTVWSNSGALTSGVHHTFPAVIQQS 60
Qy 61 GLYSLSSSVTVTPSSSLGTTOTYICNWNHKPSNTKVDKVKBPKSCDKTKHTCPPCPAPELGG 120
Db 61 GLYSLSSSVTVTPSSSLGTTOTYICNWNHKPSNTKVDKVKBPKSCDKTKHTCPPCPAPELGG 120
Qy 121 PSVFLFPKPKDITLMSRTPETVTCVWDSHEDEPKENWYTDGVEVNVKTKPREQYN 180
Db 121 PSVFLFPKPKDITLMSRTPETVTCVWDSHEDEPKENWYTDGVEVNVKTKPREQYN 180
Qy 181 STYRVISVLTVLHQNMNGKEYKCKVSNKALPAPLEKTIISKAKYQPREPQNTLPERDE 240
Db 181 STYRVISVLTVLHQNMNGKEYKCKVSNKALPAPLEKTIISKAKYQPREPQNTLPERDE 240
Qy 241 LTKNQSLTCLVKGPYPSDIAVEWESNGQPENNYKTTPVLDVGFFLYSKLTVDKSRW 300
Db 241 LTKNQSLTCLVKGPYPSDIAVEWESNGQPENNYKTTPVLDVGFFLYSKLTVDKSRW 300
Qy 301 QGNNFVCSVMEAHNNHYOQRLSLLSPGK 330
Db 301 QGNNFVCSVMEAHNNHYOQRLSLLSPGK 330

RESULT 5
 ABB81641
 ID ABB81641 standard; protein; 330 AA.
 XX AC ABB81641;
 XX DT 25-SEP-2002 (first entry)
 XX DE Human IgG gamma 1 heavy chain SEQ ID NO:15.
 XX KW Human; zcytor19; cytokine receptor; immunosuppressive; cytostatic;
 KW antiinflammatory; antiarthritic; neuroprotective; antinflammatory;
 KW anti-diabetic; nephrotropic; dermatological; anti-HIV; haemostatic;
 KW vaccine; immune system; T-cell specific; leukaemia; lymphoma; lupus;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; HIV;
 KW vasculitis; inflammatory bowel disease; Crohn's disease; asthma;
 KW immunologic renal disease; glomerular nephritis; vasculitis; polyarteritis;
 KW mesangioproliferative disease; chronic lymphocytic leukaemia; bronchitis;
 KW secondary glomerulonephritis; scleroderma; amyloidosis; multiple myeloma;
 KW haemolytic uraemic syndrome; renal neoplasm; urological neoplasm;
 KW emphysema; chronic airway disease.
 XX OS Homo sapiens.
 XX PN WO200244209-A2.
 XX PD 06-JUN-2002.
 XX ID ABB05736 standard; protein; 330 AA.
 XX PR 28-NOV-2001; 2001WO-US044808.
 XX PR 28-NOV-2000; 2000US-0251561P.
 XX PR 07-FEB-2001; 2001US-026211P.
 XX PA (ZYMO) ZYMOGENETICS INC.
 XX PI Pressnell SR, Xu W, Novak JE, Whitmore TE, Grant FU;
 XX DR WPI; 2002-522700/56.

DR N-PSDB; ABQ73076.
 XX Novel Zcytor19 polypeptides and polynucleotides useful for stimulating
 PT immune responses in animals for producing antibodies, and for treating
 PT autoimmune diseases, leukemia and asthma.
 XX Example 7; Page 171-172; 200pp; English.
 XX PS The present invention describes isolated human zcytor19 protein (I),
 CC and truncated zcytor19 proteins. (I) has immunosuppressive, cytostatic,
 CC antiinflammatory, antiarthritic, neuroprotective, antiinflammatory,
 CC anti-diabetic, nephrotropic, dermatological, anti-HIV and haemostatic
 CC activities, and can be used in vaccines. (I) or an antibody binding (I)
 CC can be used for suppressing rejection of tissue transplants and grafts and for treating T-cell specific
 CC tissue or organ transplants and grafts including rheumatoid
 CC leukaemias or lymphomas and autoimmune diseases including rheumatoid
 CC arthritis, multiple myelomas, diabetics mellitus, inflammatory bowel
 CC disease and Crohn's disease. The antibodies can also be used for treating
 CC immunologic renal diseases, glomerulonephritis, mesangioproliferative
 CC disease, chronic lymphocytic leukaemia, secondary glomerulonephritis or
 CC vasculitis associated with lupus, polyarteritis, scleroderma, HIV-related
 CC diseases, amyloidosis and haemolytic uraemic syndrome (I) and the
 CC antibodies can also be used for renal or urological neoplasms and
 CC multiple myelomas, asthma, bronchitis, emphysema and other chronic airway
 CC diseases. Human zcytor19 is located to chromosome 1, more specifically to
 CC chromosome 13q11.11. The present sequence represents a human IgG gamma 1
 CC heavy chain protein, which is used in an example from the present
 CC invention.
 XX Sequence 330 AA;
 Query Match 98.0%; Score 1729; DB 5; Length 330;
 Best Local Similarity 97.9%; Pred. No. 1.7e-122;
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 SQ **1 ASTKGPSVPLAPSSKSTSGGTAALCCLVVDYFPBPVTVWSNSGALTSGVHHTFPAVIQQS** 60
Db 1 ASTKGPSVPLAPSSKSTSGGTAALCCLVVDYFPBPVTVWSNSGALTSGVHHTFPAVIQQS 60
Qy 61 GLYSLSSSVTVTPSSSLGTTOTYICNWNHKPSNTKVDKVKBPKSCDKTKHTCPPCPAPELGG 120
Db 61 GLYSLSSSVTVTPSSSLGTTOTYICNWNHKPSNTKVDKVKBPKSCDKTKHTCPPCPAPELGG 120
Qy 121 PSVFLFPKPKDITLMSRTPETVTCVWDSHEDEPKENWYTDGVEVNVKTKPREQYN 180
Db 121 PSVFLFPKPKDITLMSRTPETVTCVWDSHEDEPKENWYTDGVEVNVKTKPREQYN 180
Qy 181 STYRVISVLTVLHQNMNGKEYKCKVSNKALPAPLEKTIISKAKYQPREPQNTLPERDE 240
Db 181 STYRVISVLTVLHQNMNGKEYKCKVSNKALPAPLEKTIISKAKYQPREPQNTLPERDE 240
Qy 241 LTKNQSLTCLVKGPYPSDIAVEWESNGQPENNYKTTPVLDVGFFLYSKLTVDKSRW 300
Db 241 LTKNQSLTCLVKGPYPSDIAVEWESNGQPENNYKTTPVLDVGFFLYSKLTVDKSRW 300
Qy 301 QGNNFVCSVMEAHNNHYOQRLSLLSPGK 330
Db 301 QGNNFVCSVMEAHNNHYOQRLSLLSPGK 330

RESULT 6
 ABB05736
 ID ABB05736 standard; protein; 330 AA.
 XX AC ABB05736;
 XX DT 01-MAY-2002 (first entry)
 XX DE Human immunoglobulin G gamma 1 protein sequence SEQ ID NO:38.
 XX KW zcytor17; chromosome 5; 5q1; cytokine receptor; immunomodulatory;
 KW antiinflammatory; antiviral; antiarthritic; immunomodulatory; cyrostatic;
 KW lymphoid; immune; inflammatory; spleenic; blood; bone;

infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease; autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer; inflammatory disease; pancreatitis; inflammatory bowel disease.

Homo sapiens

WO200200721-A2.

03-JAN-2002.

26-JUN-2001; 2001WO-US020484.

26-JUN-2000; 2000US-0214282P.
29-JUN-2000; 2000US-0214952P.
08-FEB-2001; 2001US-0267963P.

(ZMNO.) ZYMOGENETICS INC.

Sprecher CA, Pressnell SR, Gao Z, Whitmore TE, Kuijper JL,
Maurer MF;

WPI: 2002-090519/12.
N-PSDB; ABA93797.

Isolated polynucleotide encoding a cytokine receptor zcytor17 which is useful for treating and diagnosing lymphoid, immune, inflammatory, splenic, blood or bone disorders.

Example 17; Page 187-188; 235pp; English.

The present invention describes a cytokine receptor designated zcytor17. Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cyrostatic, antiarthritic, antiarthritic and muscular activities. The zcytor17 proteins are useful for treating and diagnosing lymphoid, immune, inflammatory, splenic, blood or bone disorders. As agonists or anti-zcytor17 antibodies are useful in stimulating cell-mediated immunity and for stimulating lymphocyte proliferation, such as in the treatment of infections involving immunosuppression, including certain viral infections. They are also useful for inducing cytotoxicity and for treating leukaemias. Antagonist of zcytor17 polypeptides are useful for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer, pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to chromosome 5, specifically to the 5G11 chromosomal region. ABA93767 to ABA93843 and ABB05730 to ABB05745 represent sequences used in the exemplification of the present invention

Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 5; Length 330;
Best Local Similarity 97.9%; Pred. No. 1.7e-122;

Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```

1 ASTKGPSPVPLAPSKSTSGGTAAALGLVKDYPFPEPYTVNSNGLALTSGVHTFPAVLQSS 60
1 ASTKGPSPVPLAPSKSTSGGTAAALGLVKDYPFPEPYTVNSNGLALTSGVHTFPAVLQSS 60
61 GLYSLSSTVTPSSPLGTYTICVNHKPSNTKVDKEVPKSCDKTHTCPPCPAPBLIGG 120
61 GLYSLSSTVTPSSPLGTYTICVNHKPSNTKVDKEVPKSCDKTHTCPPCPAPBLIGG 120
121 PSVFLPPPKPKDTLIMISRTPEVTCVYDVSHEDPEVKENWYDGVVEHNYTKKPREEQYN 180
121 PSVFLPPPKPKDTLIMISRTPEVTCVYDVSHEDPEVKENWYDGVVEHNYTKKPREEQYN 180
181 STYRIVSULTVLYHQNMNGKEYKCKVSNKALPAPIEKTIKAKVQPREPQYTIIPSRDE 240
181 STYRIVSULTVLYHQDWLNKEYKCKVSNKALPAPIEKTIKAKGQPREPQYTIIPSRDE 240
241 LTKQVSLTCLVKGPSPDIAVEBESNGOPENYYKTPVLDGSFLYSKLTDKSRW 300
241 LTKQVSLTCLVKGPSPDIAVEBESNGOPENYYKTPVLDGSFLYSKLTDKSRW 300

```

b

Qy 301 QGGNVFSCSYMHAEHNHYTQSLSLSPGK 330
Db 301 QGGNVFSCSYMHAEHNHYTQSLSLSPGK 330

RESULT 7
ABP71856

ID ABP71856 standard; protein; 330 AA.

XX ABP71856;

XX 17-APR-2003 (first entry)

DT XX Human IgG1 Fcgamma region.

XX Human; fusion protein; IgE Fcepsilon; IgG Fcgamma; FcepsilonRI; IgE; IgG; asthma; hay fever;

KW FcepsilonRII; Fc gammairIB; protein therapy; IgE; IgG; asthma; hay fever;

KW allergic asthma; allergic rhinitis; hay fever; food allergy;

KW atopic dermatitis; drug allergy; peanut allergen.

OS Homo sapiens.

XX Location/Qualifiers

Key PH

Region FT 1..98

/label= CH1 region

FT Region 99..113

/label= Hinge_region

FT Region 114..223

/label= CH2_region

FT Region 224..330

/label= CH3_region

XX WO2002102320-A2.

XX PD 27-DEC-2002.

XX PF 14-JUN-2002; 2002WO-US019448.

XX PR 15-JUN-2001; 2001US-0298710P.

XX PA (TANCO-) TANOX INC.

XX PI An L, Wu H, Fung MSC;

XX DR 2003-167440/16.

XX New fusion protein which binds to FcepsilonRI or RII receptor and PT Fc gamma RII receptor, useful for treating or preventing allergies and

PT asthma, comprises an IgG Fc gamma fragment.

XX Disclosure; Fig 5; 32pp; English.

CC The invention relates to a novel fusion protein comprising an IgE

CC Fc epsilon fragment and an IgG Fc gamma fragment, which binds to an

CC Fc epsilon RI and/or Fc epsilon RII receptor, and an Fc gamma RII receptor. The

CC fusion protein of the invention may have a use in protein therapy. The

CC fusion protein is useful in treating or preventing IgE-mediated allergies

CC and asthma, such as allergic asthma, allergic rhinitis, hay fever, food

CC allergy, atopic dermatitis and drug allergy. The allergic response is

CC particularly caused by peanut allergen. The present sequence represents

CC the human IgG1 Fc gamma fragment.

XX Sequence 330 AA;

SQ Query Match 98.0%; Score 1729; DB 6; Length 330;

Best Local Similarity 97.9%; Pred. No. 1.7e-122;

Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSPVPLAPSKSTSGGTAAALGLVKDYPFPEPYTVNSNGLALTSGVHTFPAVLQSS 60

Db 1 ASTKGPSPVPLAPSKSTSGGTAAALGLVKDYPFPEPYTVNSNGLALTSGVHTFPAVLQSS 60

Qy 61 GLYSLSSTVTPSSPLGTYTICVNHKPSNTKVDKEVPKSCDKTHTCPPCPAPBLIGG 120

Db 61 GLYSLSSTVTPSSPLGTYTICVNHKPSNTKVDKEVPKSCDKTHTCPPCPAPBLIGG 120

Qy 121 PSVFLPPPKPKDTLIMISRTPEVTCVYDVSHEDPEVKENWYDGVVEHNYTKKPREEQYN 180

Db 121 PSVFLPPPKPKDTLIMISRTPEVTCVYDVSHEDPEVKENWYDGVVEHNYTKKPREEQYN 180

Qy 181 STYRIVSULTVLYHQNMNGKEYKCKVSNKALPAPIEKTIKAKVQPREPQYTIIPSRDE 240

Db 181 STYRIVSULTVLYHQDWLNKEYKCKVSNKALPAPIEKTIKAKGQPREPQYTIIPSRDE 240

Qy 241 LTKQVSLTCLVKGPSPDIAVEBESNGOPENYYKTPVLDGSFLYSKLTDKSRW 300

Db 241 LTKQVSLTCLVKGPSPDIAVEBESNGOPENYYKTPVLDGSFLYSKLTDKSRW 300

Qy 61 GLYSLSSTVTPSSPLGTYTICVNHKPSNTKVDKEVPKSCDKTHTCPPCPAPBLIGG 120

Db 61 GLYSLSSTVTPSSPLGTYTICVNHKPSNTKVDKEVPKSCDKTHTCPPCPAPBLIGG 120

Query Match 98.0%; Score 1729; DB 6; Length 330;
 Best Local Similarity 97.9%; Pred. No. 1.7e-122;
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 ASTKGPSPVFLAPSKSSTSGGTAALGLCLVQDYFPBPVTSWNSGALTGGYHTPAVLOSS 60
 1 ASTKGPSPVFLAPSKSSTSGGTAALGLCLVQDYFPBPVTSWNSGALTGGYHTPAVLOSS 60

61 GLYSLSSVVTPSSSLGTTQTYTICNWNHKPSNTKVDCKVEPKSCDTHTCPPCPAPELLGG 120
 61 GLYSLSSVVTPSSSLGTTQTYTICNWNHKPSNTKVDCKVEPKSCDTHTCPPCPAPELLGG 120

121 PSVLFPPFKPDKDTLMISRTPPEVTKFENYVDGEVENVTKTKEPEEQYN 180
 121 PSVLFPPFKPDKDTLMISRTPPEVTKFENYVDGEVENVTKTKEPEEQYN 180

181 STRYVVSUTIVHQNMNGKEYKCKVSNKALPAPLEKTISKAKVPRECPVYTLPPSRDE 240
 181 STRYVVSUTIVHQDWINGKEYKCKVSNKALPAPLEKTISKAKGPRECPVYTLPPSRDE 240

241 LTQNQVSLTCLVKGFYPSDIAVENSQOPENNYKTPVLDSDGSFELYSKLTVDSRW 300
 241 LTQNQVSLTCLVKGFYPSDIAVENSQOPENNYKTPVLDSDGSFELYSKLTVDSRW 300

301 QQGNVFCSVMHEALHNHYQQESLSSPGK 330
 301 QQGNVFCSVMHEALHNHYQQESLSSPGK 330

SU71.0
 R82103 standard; protein; 330 AA.
 ABB82103 ;
 23-SEP-2003 (first entry)
 Human DR6 related amino acid sequence SEQ ID NO:5.

Human: DR6; B-cell mediated disease; immunosuppressive; antirheumatic; antiarthritic; antiasthmatic; dermatologic; antiflammatory; antithyroid; nephrotropic; antiinfective; cytostatic; neuroprotective; thymomimetic; hepatotropic; antibacterial; antiulcer; haemostatic; antiaemic; antimicrobial; anti-HIV; DR6 antagonist; immunity.

Hom sapiens
 WO200301290-A2.
 26-JUN-2003.
 10-DEC-2002; 2002WO-US037596.
 17-DEC-2001; 2001US-0342632P.
 (ELIL) LILLY & CO ELI.
 Liu J, Na S, Song HY, Yang D;
 WPI; 2003-541604/51.

administering a pharmaceutical composition comprising at least one DR6 agonist; (2) use of DR6 agonist in the manufacture of a medicament for treating or preventing at least one symptom associated with conditions (C1) such as aberrant apoptosis, graft-versus-host disease (GVHD), atopy, rheumatoid arthritis, asthma, inflammatory bowel disease, cancer, vasculitis, psoriasis, insulin-dependent diabetes mellitus, pancytopenia, multiple sclerosis, Hashimoto's thyroiditis, Graves' disease, transplant rejection, systemic lupus erythematosus, Behcet's disease, autoimmune nephropathy, autoimmunity haemoptysis, idiopathic interstitial pneumonitis, hypersensitivity pneumonitis, autoimmune gastritis, autoimmune cardiopathy, autoimmune infertility, autoimmune hepatitis B, fulminant viral fibrosis, lung disease, fulminant viral hepatitis, chronic cirrhosis, autoimmune hepatitis, chronic hepatitis, organ refection after helicobacter pylori associated ulceration, organ transplantation, chronic glomerulonephritis, thrombotic thrombocytopenic purpura (TTP) and haemolytic uraemic syndrome (HUS), plastic anaemia, myelodysplasia, multiple organ dysfunction syndrome (MDS), adult respiratory distress syndrome (ARDS), and at least one condition or hepatitis C, autoimmune hepatitis, chronic hepatitis, bacterial infection, purpura (TTP) and haemolytic uraemic syndrome (HUS), HIV-induced lymphoma, HIV-induced AIDS, fulminant viral hepatitis B, fulminant viral hepatitis C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis, H. pylori-associated ulceration, cycloprotection during cancer treatment, recuperation from chemotherapy, recuperation from irradiation therapy, and at least one condition or symptom related to the conditions in a mammal, DR6 has immunosuppressive, antirheumatic, antiarthritic, antiasthmatic, dermatological, antiinflammatory, antipsoriatic, antidiabetic, cytosstatic, neuroprotective, thymomimetic, antithyroid, nephrotropic, antiinfective, cytostatic, neuroprotective, hepatotropic, nephrotropic, antineoplastic, virucide, hepatotoxic, antimicrobial, antibacterial, antiulcer, haemostatic, antiaemic, antimicrobial and anti-HIV activities. (M1) is useful for treating or preventing at least one symptom associated with (C1) in a mammal, preferably human, by administering DR6 agonist, and for treating or preventing at least one symptom associated with (C2) by administering DR6 antagonist. The present sequence represents a human DR6 antagonist. The present sequence given in the exemplification of the present invention

Sequence 330 AA:

Query Match 98.0%; Score 1729; DB 6; Length 330;
 Best Local Similarity 97.9%; Pred. No. 1.7e-122;
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 ASTKGPSVFPFLAPSKSSTSGGTAALGLCLVQDYFPBPVTSWNSGALTGGYHTPAVLOSS 60
 1 ASTKGPSVFPFLAPSKSSTSGGTAALGLCLVQDYFPBPVTSWNSGALTGGYHTPAVLOSS 60

61 GLYSLSSVVTPSSSLGTTQTYTICNWNHKPSNTKVDCKVEPKSCDTHTCPPCPAPELLGG 120
 61 GLYSLSSVVTPSSSLGTTQTYTICNWNHKPSNTKVDCKVEPKSCDTHTCPPCPAPELLGG 120

121 PSVLFPPFKPDKDTLMISRTPPEVTKFENYVDGEVENVTKTKEPEEQYN 180
 121 PSVLFPPFKPDKDTLMISRTPPEVTKFENYVDGEVENVTKTKEPEEQYN 180

181 STRYVVSUTIVHQNMNGKEYKCKVSNKALPAPLEKTISKAKVPRECPVYTLPPSRDE 240
 181 STRYVVSUTIVHQDWINGKEYKCKVSNKALPAPLEKTISKAKGPRECPVYTLPPSRDE 240

241 LTQNQVSLTCLVKGFYPSDIAVENSQOPENNYKTPVLDSDGSFELYSKLTVDSRW 300
 241 LTQNQVSLTCLVKGFYPSDIAVENSQOPENNYKTPVLDSDGSFELYSKLTVDSRW 300

301 QQGNVFCSVMHEALHNHYQQESLSSPGK 330
 301 QQGNVFCSVMHEALHNHYQQESLSSPGK 330

RESULT 11
 AAO31102

ID	AAC31102	standard; protein; 330 AA.	XX	XX	ABR55836;
XX	AC		XX	XX	
XX	ABO31102;		DT	02-SEP-2003	(first entry)
XX	06-OCT-2003	(first entry)	XX	XX	
DB	Human A2-G8 SCF antibody heavy chain constant region.		DE	Anti-Ang-2 antibody IgG1 constant region.	
XX			XX	XX	
XX	Human; antibody; stem cell factor; mast cell growth factor; asthma; SCF;		KW	Ang-2; angiopoietin-2; anorectic; cytostatic; antiarteriosclerotic;	
KW	Human; antibody; stem cell factor; mast cell growth factor; asthma; SCF;		KW	gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;	
KW	c-kit ligand; gene therapy; heavy chain.		KW	angiogenesis; antibody; human.	
XX			XX	XX	
OS	Homo sapiens.		OS	Homo sapiens.	
XX			XX	XX	
PN	WO2003051311-A2.		PN	WO2003030833-A2.	
XX			XX	XX	
PD	26-JUN-2003.		PD	17-APR-2003.	
XX			XX	XX	
PF	16-DEC-2002; 2002WO-US040227.		PF	11-OCT-2002; 2002WO-US032613.	
XX			XX	XX	
PR	17-DEC-2001; 2001US-0342174P.		PR	11-OCT-2001; 2001US-0328604P.	
XX			PR	10-OCT-2002; 2002US-00269805.	
PA	(FARB) BAYER CORP.		PA	(AMGEN-) AMGEN INC.	
XX			XX	XX	
PI	Takeuchi T, Tomkinson A, Neben S;		PI	Oliner JD;	
XX			XX	XX	
DR	WPI; 2003-523500/49.		DR	WPI; 2003-504963/47.	
N-PSDB;	AAU62618.		PS	Example 4; Page 96; 161pp; English.	
XX			XX	PT	New specific binding agents (i.e. anti-Angiopoietin-2 antibodies), useful for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity, hemangioma, arteriosclerosis, atherosclerosis, or endometriosis.
PS	New purified human antibody that binds to stem cell factor protein, useful for preparing a composition for treating asthma.		XX	PT	The invention relates to a specific binding agent, which comprises at least one peptide selected from any of 62 peptides (ABR55769-80) or its fragment. The binding agents are antibodies that recognize and bind to angiopoietin-2 (Ang-2). The specific binding agent, particularly the antibody, is useful for inhibiting undesired angiogenesis, treating cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-2 activity, modulating vascular permeability or plasma leakage, or treating a disease (e.g. ocular neovascular disease, obesity, haemangioblastoma, haemangioma, arterioocclusive disease, inflammatory disorders, atherosclerosis, neoplastic, endometriosis, bone-related disease, or psoriasis) in a mammal. The present sequence represents a human IgG1 constant region of an anti-Ang-2 antibody.
XX			XX	XX	Example 4; Page 96; 161pp; English.
PS	Example 10; Page 47-48; 94pp; English.		PS	Sequence 330 AA;	
XX			XX	Query Match 98.0%; Score 1729; DB 6; Length 330;	
CC	The invention provides human antibodies that bind to stem cell factor (SCF) protein. SCF is also known as mast cell growth factor, steel factor or c-kit ligand. Antibodies of the invention are useful for preparing compositions for treating asthma. They are also used in gene therapy. The present sequence is human SCF antibody heavy chain constant region.		Best Local Similarity 97.9%; Pred. No. 1.7e-122;	Best Local Similarity 97.9%; Pred. No. 1.7e-122;	
CC			Matches 3; Mismatches 3; Conservative 3; Indels 0; Gaps 0;	Matches 3; Mismatches 3; Conservative 3; Indels 0; Gaps 0;	
CC			Qy 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Qy 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Db 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Db 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Qy 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Qy 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Db 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Db 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Qy 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Qy 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Db 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Db 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Qy 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Qy 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Db 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Db 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Qy 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Qy 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Db 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Db 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Qy 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Qy 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Db 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Db 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Qy 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Qy 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Db 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Db 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Qy 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Qy 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Db 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Db 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Qy 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Qy 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Db 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Db 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Qy 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Qy 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Db 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Db 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Qy 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Qy 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Db 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Db 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Qy 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Qy 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Db 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Db 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Qy 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Qy 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Db 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Db 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Qy 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Qy 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
CC			Db 1 ASTKGGSVFPAPSSKSTSGSTAALGCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	Db 1 ASTKGPSUEPLAPSXSKTSGGTANLCLVYDYPPEPTVWSNGALISGVHTFPAVLQSS 60	
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CC		</td			

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Db 301 QOGNVFSCSYVMHEALTHNHYQRSLSLSPGK 330
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SULT 13
 AA030893 standard; protein; 330 AA.

RESULT 14
 ADF11389 standard; protein; 330 AA.
 ID ADF11389
 XX
 AC ADF11389;
 XX
 DT 12-FEB-2004 (first entry)
 DE Anti-OPGL antibody heavy chain constant region SEQ ID NO:2.
 XX
 KW human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
 KW osteopathic; antiarthritic; cyostatic; gene therapy; bone disorder;
 KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.
 XX
 DE Homo sapiens.
 XX
 OS Homo sapiens.
 XX
 PN WO2003086289-A2.
 XX
 PD 23-OCT-2003.
 XX
 PF 07-APR-2003; 2003WO-US010749.
 XX
 PR 05-APR-2002; 2002US-0370407P.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PT Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;
 XX
 PT WPI; 2003-B45253/78.
 DR N-PSDB; ADF11388.
 XX
 PT New isolated antibody that specifically binds osteoprotegerin ligand,
 PT useful for diagnosing or treating bone disorders, such as osteoporosis,
 PT bone loss from arthritis, Paget's disease or osteopenia.
 XX
 Example 3: SEQ ID NO 2; 156pp; English.
 PS The present invention describes an isolated human antibody (I) that
 CC specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a
 CC pharmaceutical composition comprising a pharmaceutical carrier and a
 CC therapeutic amount of (I); (2) methods of treating an osteopenic disorder
 CC in a patient, comprising administering to a patient the pharmaceutical
 CC composition of (1) or a pharmaceutical amount of (1); and (3) a method
 CC for detecting OPGL in a biological sample, comprising contacting the
 CC sample with (I) under conditions that allow for binding of the antibody
 CC to OPGL, and measuring the level of bound antibody in the sample. (I) has
 CC osteopathic, antiarthritic and cyostatic activities, and can be used in
 CC gene therapy. The composition and methods are useful in diagnosing or
 CC treating bone disorders, such as osteoporosis, bone loss from arthritis,
 CC Paget's disease or osteopenia. The antibody (I) may also be used for
 CC detecting OPGL in biological samples and in identifying cells or tissues
 CC that produce the protein. The present sequence represents a sequence
 CC which is used in the exemplification of the present invention.
 XX
 SQ Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 6; Length 330;
 Best Local Similarity 97.9%; Pred. No. 1..7e-12;
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 ASTKGPSVFLPAPSXSKSTSGGTAAIGLVKDYFPEPTVWSNSGALTSGVHTFPAVLQSS 60
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 2 GLYSLSVVTVPSSSLGTQTYICNINHKSNTKVDKKVEPKESCDKTHTCPPCPAPLLGG 120
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 2 GLYSLSVVTVPSSSLGTQTYICNINHKSNTKVDKKVEPKESCDKTHTCPPCPAPLLGG 120
 2 GLYSLSVVTVPSSSLGTQTYICNINHKSNTKVDKKVEPKESCDKTHTCPPCPAPLLGG 120
 1 PSVFLPKEPKDTMISRPETVTVNDLSDHEDEKVNWTGQEVHANVTKPQEQQN 180
 1 PSVFLPKEPKDTMISRPETVTVNDLSDHEDEKVNWTGQEVHANVTKPQEQQN 180
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 1 STRYVSVTVLQHQNWNMGKEYKCRVSNKALPATEKTIKAKVQPQEPQVYLPSRDE 240

Query Match 98.0%; Score 1729; DB 7; Length 330;
 Best Local Similarity 97.9%; Pred. No. 1..7e-12;
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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GenCore version 5.1.6
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protein - protein search, using sw model

on: October 27, 2004, 17:04:05 ; Search time 100.936 Seconds

(without alignments)

1059.356 Million cell updates/sec

tile: US-10-000-439-2

ffect score: 1764

quence: 1 ASTKGPSVPLAPSSKSTSG.....NHEALTHHYQORSISLSLSPGK 330

oring table: BLASTM62

Gapext 0.5

arched: 1370721 seqs, 32421580 residues

tal number of hits satisfying chosen parameters: 1370721

nimum DB seq length: 0

ximum DB seq length: 2000000000

st-processing: Maximum Match 0%

Listing first 45 summaries

atabase : Published Applications AA: *

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20: /cgn2_6/ptodata/1/pubpa/us560_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Match Length	DB ID	Description
1	1764	100.0	330 10 US-09-847-208-2	Sequence 2, Appli
2	1764	100.0	330 14 US-10-000-439-2	Sequence 2, Appli
3	1729	98.0	330 10 US-09-995-898A-15	Sequence 15, Appli
4	1729	98.0	330 10 US-09-892-949-38	Sequence 38, Appli
5	1729	98.0	330 13 US-10-047-542-20	Sequence 20, Appli
6	1729	98.0	330 14 US-10-269-805-68	Sequence 68, Appli
7	1729	98.0	330 14 US-10-310-719-8	Sequence 8, Appli
8	1729	98.0	330 14 US-10-112-582-1	Sequence 1, Appli
9	1729	98.0	330 14 US-10-320-231A-81	Sequence 81, Appli
10	1729	98.0	330 14 US-10-383-902A-6	Sequence 6, Appli
11	1729	98.0	330 15 US-10-408-901-2	Sequence 2, Appli
12	1729	98.0	330 15 US-10-420-030A-15	Sequence 15, Appli
13	1729	98.0	330 15 US-10-257-907A-5	Sequence 5, Appli

14	1729	98.0	330 15 US-10-656-769-2	Sequence 2, Appli
15	1729	98.0	330 16 US-10-772-531-38	Sequence 38, Appli
16	1729	98.0	332 10 US-11-0-479-326-1	Sequence 1, Appli
17	1729	98.0	332 10 US-13-990-586-98	Sequence 98, Appli
18	1729	98.0	332 14 US-10-310-113-167	Sequence 167, Appli
19	1729	98.0	332 14 US-10-230-880-98	Sequence 98, Appli
20	1729	98.0	333 15 US-10-272-898A-72	Sequence 72, Appli
21	1729	98.0	336 15 US-10-157-408-7	Sequence 7, Appli
22	1729	98.0	371 14 US-10-097-04A-7	Sequence 7, Appli
23	1729	98.0	371 14 US-10-320-231A-79	Sequence 7, Appli
24	1729	98.0	371 17 US-10-320-231A-79	Sequence 12, Appli
25	1729	98.0	442 15 US-10-225-435-12	Sequence 12, Appli
26	1729	98.0	442 17 US-10-487-322-12	Sequence 6, Appli
27	1729	98.0	444 14 US-10-150-475A-16	Sequence 6, Appli
28	1729	98.0	444 16 US-10-704-522-6	Sequence 6, Appli
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30	1729	98.0	445 14 US-10-408-901-50	Sequence 50, Appli
31	1729	98.0	445 15 US-10-408-901-34	Sequence 7, Appli
32	1729	98.0	445 15 US-10-408-901-42	Sequence 42, Appli
33	1729	98.0	446 15 US-10-408-901-40	Sequence 30, Appli
34	1729	98.0	446 15 US-10-408-901-38	Sequence 38, Appli
35	1729	98.0	446 15 US-10-408-901-46	Sequence 46, Appli
36	1729	98.0	446 15 US-10-435-299-7	Sequence 5, Appli
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39	1729	98.0	448 15 US-10-78-5-7-2	Sequence 2, Appli
40	1729	98.0	451 9 US-09-822-998A-16	Sequence 26, Appli
41	1729	98.0	453 17 US-10-813-483-5	Sequence 6, Appli
42	1729	98.0	467 15 US-10-108-260-2	Sequence 4293, Appli
43	1729	98.0	467 15 US-10-656-169-72	Sequence 34, Appli
44	1729	98.0	469 15 US-10-656-769-20	Sequence 20, Appli
45	1729	98.0	469 15 US-10-656-769-26	Sequence 26, Appli

ALIGNMENTS

RESULT 1	Query Match	100.0%	Score 1764;	DB 10;	Length 330;
	Best Local Similarity	100.0%	Pred. No. 1.2e-128;		
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					Gaps 0;
US-09-847-208-2	1 ASTKGPSVPLAPSSKSSTGGTAALGCLVVDYFPEPVTVNSGALTSGVHTFPVAVQGS				
	Publication No. US00300802190A1				
	GENERAL INFORMATION:				
	SEQUENCE 2, Application US/09847208				
	APPLICATION: Saxon, Andrew				
	APPLICANT: Zhang, Ke				
	APPLICANT: Zhu, Daoheng				
	TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF				
	FILE REFERENCE: UC67 002A				
	CURRENT APPLICATION NUMBER: US/09/847,208				
	CURRENT FILING DATE: 2001-05-01				
	NUMBER OF SEQ ID NOS: 177				
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	LENGTH: 330				
	TYPE: PRT				
	ORGANISM: Homo sapiens				
US-09-847-208-2					

APPLICANT: Grant, Francis J. CYTOKINE RECEPTOR ZCYTOR19
 TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
 FILE REFERENCE: 00-08
 CURRENT APPLICATION NUMBER: US/09/95,898A
 CURRENT FILING DATE: 2001-11-28
 PRIORITY APPLICATION NUMBER: US 60/253,561
 PRIORITY FILING DATE: 2000-11-28
 PRIORITY FILING DATE: 2001-02-07
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 15
 LENGTH: 330
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-095-898A-15

RESULT 2
 US-10-000-439-2
 Sequence 2, Application US/10000439
 Publication No. US2003006403A1.
 GENERAL INFORMATION:
 APPLICANT: Saxon, Andrew
 TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
 TREATMENT OF IMMUNE DISEASES
 FILE REFERENCE: UC067-004A
 CURRENT APPLICATION NUMBER: US/10/000,439
 CURRENT FILING DATE: 2001-10-24
 PRIORITY APPLICATION NUMBER: US 09/847,208
 PRIORITY FILING DATE: 2001-05-01
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 2
 LENGTH: 330
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-000-439-2

Query Match 98.0%; Score 1729; DB 110; Length 330;
 Best Local Similarity 97.9%; Pred. No. 6.4e-126;
 Mismatches 3; Indels 0; Gaps 0;

Matches 323; Conservative 3; MisMatches 0; Qy 1 ASTKGPSVPLAPS SKTSGGTAALGCLVQDYFPEPVTVSNNSGALTSGVHTFPVAVLOSS 60
 Db 1 ASTKGPSVPLAPS SKTSGGTAALGCLVQDYFPEPVTVSNNSGALTSGVHTFPVAVLOSS 60

Qy 61 GLYLSVVTVTPSSSLGQTQYICNWNHKPSNTKVDKVEPKSCDCKHTCPCPAPELGG 120
 Db 61 GLYLSVVTVTPSSSLGQTQYICNWNHKPSNTKVDKVEPKSCDCKHTCPCPAPELGG 120

Qy 121 PSVFLFPPKPKDTLMISRTPETCVVYDVSHEDPEVKPENNYDGVYEVHNVTKRPREQYN 180
 Db 121 PSVFLFPPKPKDTLMISRTPETCVVYDVSHEDPEVKPENNYDGVYEVHNVTKRPREQYN 180

Qy 161 STYRVSVLTVLHQINNGKEYKCKVSKNKLAPAPIEKTISKAKVQPREPQVTLPPSRDE 240
 Db 161 STYRVSVLTVLHQDWLNGKEYKCKVSKNKLAPAPIEKTISKAKGPREPVYTLPPSRDE 240

Qy 241 LTKNOVSUTCLVKGFYPSDIATEWESNGOPENNNYKTPPPVLDSSGSEFLYSKLTVDKSRW 300
 Db 241 LTKNOVSUTCLVKGFYPSDIATEWESNGOPENNNYKTPPPVLDSSGSEFLYSKLTVDKSRW 300

Qy 301 QQNVFCSVMHBAHNHYQRSLSLSPGK 330
 Db 301 QQNVFCSVMHBAHNHYQRSLSLSPGK 330

RESULT 4
 US-09-898A-15
 Sequence 38, Application US/09892949
 Publication No. US2003009633A1
 GENERAL INFORMATION:
 APPLICANT: Sprecher, Cindy A.
 APPLICANT: Presnell, Scott R.
 APPLICANT: Gao, Zeren
 APPLICANT: Whitmore, Theodore E.
 APPLICANT: Kuijper, Joseph L.
 APPLICANT: Maurer, Mark F.
 TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
 FILE REFERENCE: 00-42
 CURRENT FILING DATE: 2001-06-26
 PRIORITY APPLICATION NUMBER: US 60/214,282
 PRIORITY FILING DATE: 2000-06-29
 PRIORITY FILING DATE: 2000-06-29
 NUMBER OF SEQ ID NOS: 93
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 38
 LENGTH: 330
 TYPE: PRT
 ORGANISM: Homo sapiens

RESULT 3
 US-09-995-898A-15
 Sequence 15, Application US/09995698A
 Publication No. US2003002725A1
 GENERAL INFORMATION:
 APPLICANT: Presnell, Scott R.
 APPLICANT: Xu, Wenfang
 APPLICANT: No. US200302725A1ak, Julia E.
 APPLICANT: Whitmore, Theodore E.

09-892-949-38

Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVTLPSPRDE 240

Qy 241 LTKNOVSITCLVKGFPSIDAVENGOPENNYKTTPVLDGSFFFLYSKLTVDSKRW 300

Db 241 LTKNOVSITCLVKGFPSIDAVENGOPENNYKTTPVLDGSFFFLYSKLTVDSKRW 300

Qy 301 QGNYFSCSYNHEALTHHYQORSLSLSPGK 330

Db 301 QGNYFSCSYNHEALTHHYTQKSLSLSPGK 330

RESULT 6

US-10-269-805-68

; Sequence 68, Application US/10269805

; Publication No. US2003012419A1

; GENERAL INFORMATION:

; APPLICANT: OLINER, JONATHAN D.

; TITLE OF INVENTION: ANGIOPLETIN-2 SPECIFIC BINDING AGENTS

; FILE REFERENCE: A-722

; CURRENT APPLICATION NUMBER: US/10/269,805

; CURRENT FILING DATE: 2002-10-10

; PRIOR APPLICATION NUMBER: US 60/328,604

; PRIOR FILING DATE: 2001-10-11

; NUMBER OF SEQ ID NOS: 76

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO: 68

; LENGTH: 330

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-269-805-68

Query Match 98.0%; Score 1729; DB 14; Length 330;

Best Local Similarity 97.9%; Pred. No. 6.4e-126;

Matches 3; Mismatches 4; Indels 0; Gaps 0;

SULT 5

-10-047-542-20

Sequence 20, Application US/10047542

Publication No. US20020168367A1

GENERAL INFORMATION:

APPLICANT: LARRICK, JAMES W.

APPLICANT: WYCOFF, KEITH L.

TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL

FILE REFERENCE: 0120905_0004_CIP1

CURRENT FILING DATE: 2001-10-26

PRIOR APPLICATION NUMBER: PCT/US01/13932

PRIOR FILING DATE: 2001-04-28

PRIOR APPLICATION NUMBER: 60/200,298

PRIOR FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 101

SEQ ID NO: 20

LENGTH: 330

TYPE: PRT

ORGANISM: Homo sapiens

-10-047-542-20

Query Match 98.0%; Score 1729; DB 13; Length 330;

Best Local Similarity 97.9%; Pred. No. 6.4e-126;

Matches 3; Mismatches 4; Indels 0; Gaps 0;

SULT 7

US-10-310-719-8

; Sequence 8, Application US/10310719

; Publication No. US20030166163A1

; GENERAL INFORMATION:

; APPLICANT: Gillies, Stephen

; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity

; FILE REFERENCE: LEX-020

; CURRENT APPLICATION NUMBER: US/10/310,719

; CURRENT FILING DATE: 2003-12-04

; PRIOR APPLICATION NUMBER: 60/337,113

; PRIOR FILING DATE: 2001-12-04

; PRIOR APPLICATION NUMBER: 60/371,966

1 ASTKGPSIPLAPSSKSSTSGGTAALGCKDFFPEPVTVWSNSGALTSGVHTFPVLOSS 60

1 ASTKGPSIPLAPSSKSSTSGGTAALGCKDFFPEPVTVWSNSGALTSGVHTFPVLOSS 60

61 GLYLSSSVTVPSLGLQTOTYICNVNHPKSNKVDKKEPKSCDKTHTCPGPAPLLGG 120

61 GLYLSSSVTVPSLGLQTOTYICNVNHPKSNKVDKKEPKSCDKTHTCPGPAPLLGG 120

121 PSVLFPPXPKDLMISRPTEVTCVVWDVSHDEPEVKFNWYTDGVENVTKTPREQYN 180

121 PSVLFPPXPKDLMISRPTEVTCVVWDVSHDEPEVKFNWYTDGVENVNAKTKTPREQYN 180

181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVTLPSPRDE 240

Qy 301 QGNYFSCSYNHEALTHHYQORSLSLSPGK 330

Qy 301 QGNYFSCSYNHEALTHHYTQKSLSLSPGK 330

RESULT 7

US-10-310-719-8

; Sequence 8, Application US/10310719

; Publication No. US20030166163A1

; GENERAL INFORMATION:

; APPLICANT: Gillies, Stephen

; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity

; FILE REFERENCE: LEX-020

; CURRENT APPLICATION NUMBER: US/10/310,719

; CURRENT FILING DATE: 2003-12-04

; PRIOR APPLICATION NUMBER: 60/337,113

; PRIOR FILING DATE: 2001-12-04

; PRIOR APPLICATION NUMBER: 60/371,966

PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 8
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc
; LOCATION: (1..(330))
; OTHER INFORMATION: IgG1 constant region
US-10-310-719-8

Query Match 98.0%; Score 1729; DB 14; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.4e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVPLAPSSKSTGGTAALGCLVKDYFPEPVTVWSNSGALTSGVHTRPAVLQSS 60
Db 1 ASTKGPSVPLAPSSKSTGGTAALGCLVKDYFPEPVTVWSNSGALTSGVHTRPAVLQSS 60

Qy 61 GLYLSSSVTVSSGIGTQTYICNVNHPKSNTKYDKVKEPKSCDKTHTCPGPAPELGG 120
Db 61 GLYLSSSVTVSSGIGTQTYICNVNHPKSNTKYDKVKEPKSCDKTHTCPGPAPELGG 120

Qy 121 PSVFLPPRKPKDTLMSRTPETVTCVVDYSHEDPEVKENWYDVGVEVNAKTKPREEQYN 180
Db 121 PSVFLPPRKPKDTLMSRTPETVTCVVDYSHEDPEVKENWYDVGVEVNAKTKPREEQYN 180

Qy 181 STYRVVSVLTVLHQINNGKEYKCKVSNKALPAPIEKTISKAKYQPREQVTLPSSRDE 240
Db 181 STYRVVSVLTVLHQINNGKEYKCKVSNKALPAPIEKTISKAKYQPREQVTLPSSRDE 240

Qy 241 LTKNOVSLSLTCLVKGFYPSDIAVEWSNGOPENNYKTPVLDGSFFLYSKLTVDKSRW 300
Db 241 LTKNOVSLSLTCLVKGFYPSDIAVEWSNGOPENNYKTPVLDGSFFLYSKLTVDKSRW 300

Qy 301 QCGNVFSCSYVHEALTHYHQYRSISLSLSPGK 330
Db 301 QCGNVFSCSYVHEALTHYHQYRSISLSLSPGK 330

RESULT 8
US-10-112-582-1

; Sequence 1. Application US/10112582
; Publication No. US2003016687A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
; FILE REFERENCE: LEX-017
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/280,625
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 1
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: human Ig gamma heavy chain C region
US-10-112-582-1

Query Match 98.0%; Score 1729; DB 14; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.4e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVPLAPSSKSTGGTAALGCLVKDYFPEPVTVWSNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVPLAPSSKSTGGTAALGCLVKDYFPEPVTVWSNSGALTSGVHTFPAVLQSS 60

Qy 61 GLYLSSSVTVSSGIGTQTYICNVNHPKSNTKYDKVKEPKSCDKTHTCPGPAPELGG 120
Db 61 GLYLSSSVTVSSGIGTQTYICNVNHPKSNTKYDKVKEPKSCDKTHTCPGPAPELGG 120

Qy 121 PSVFLPPRKPKDTLMSRTPETVTCVVDYSHEDPEVKENWYDVGVEVNAKTKPREEQYN 180
Db 121 PSVFLPPRKPKDTLMSRTPETVTCVVDYSHEDPEVKENWYDVGVEVNAKTKPREEQYN 180

Qy 181 STYRVVSVLTVLHQINNGKEYKCKVSNKALPAPIEKTISKAKYQPREQVTLPSSRDE 240
Db 181 STYRVVSVLTVLHQINNGKEYKCKVSNKALPAPIEKTISKAKYQPREQVTLPSSRDE 240

Qy 241 LTKNOVSLSLTCLVKGFYPSDIAVEWSNGOPENNYKTPVLDGSFFLYSKLTVDKSRW 300
Db 241 LTKNOVSLSLTCLVKGFYPSDIAVEWSNGOPENNYKTPVLDGSFFLYSKLTVDKSRW 300

Qy 301 QCGNVFSCSYVHEALTHYHQYRSISLSLSPGK 330
Db 301 QCGNVFSCSYVHEALTHYHQYRSISLSLSPGK 330

SULT 10 -10-383-902A-6 Sequence 6, Application US/10383902A
 Publication No. US20030224408A1
 GENERAL INFORMATION:
 APPLICANT: Hogenboom, Henricus Renerus Jacobus Mattheus
 APPLICANT: Mulberg, Robert C.
 TITLE OF INVENTION: LIGAND SCREENING AND DISCOVERY
 FILE REFERENCE: 10280-42001
 CURRENT APPLICATION NUMBER: US 60/383,902A
 CURRENT FILING DATE: 2003-03-07
 PRIOR APPLICATION NUMBER: US 60/362,403
 PRIOR FILING DATE: 2002-01-07
 NUMBER OF SEQ ID NOS: 58
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 6
 LENGTH: 330
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: synthetically generated plasmid sequence
 -10-383-902A-6

Query Match	Score	DB 14;	Length 330;
Best Local Similarity	97.9%	Pred. No. 6.4e-126;	
Matches 323;	Conservative	N mismatches 4;	Indels 0;
		Gaps 0;	
1 ASTKGPSVFPAPSSKSTSGGTAALCGLVYDFPBPFTVWSNSGALTSGVHTFPAVLQSS	60		
1 ASTKGPSVFPAPSSKSTSGGTAALCGLVYDFPBPFTVWSNSGALTSGVHTFPAVLQSS	60		
61 GLYSLSVVTVYPPSSIGTQTYICNVNHPKSNTKVDKVKVEPKSDCXTHTCPPCPAPELIGG	120		
61 GLYSLSVVTVYPPSSIGTQTYICNVNHPKSNTKVDKVKVEPKSDCXTHTCPPCPAPELIGG	120		
121 PSVFLPPKPDKDTLMISRPEVTKVVDVSHEDPEKTFENWVTDGVFHVNVTKPREEQIN	180		
121 PSVFLPPKPDKDTLMISRPEVTKVVDVSHEDPEKTFENWVTDGVFHVNVTKPREEQIN	180		
181 STYRVSVLTVLHQDWYNGKEYKCKVYSKNSKALPAPIKTISKAKVOPREPOVYTLPSPRDE	240		
181 STYRVSVLTVLHQDWYNGKEYKCKVYSKNSKALPAPIKTISKAKVOPREPOVYTLPSPRDE	240		
241 LTQNQSLTCLVKGFPSDIAVEWENGOPENNYKTPPVYLDVSGFFLYSKLTVDKSRW	300		
241 LTQNQSLTCLVKGFPSDIAVEWENGOPENNYKTPPVYLDVSGFFLYSKLTVDKSRW	300		
301 QQQNPFCSWMEAHLYQPSLSSLSPGK	330		
301 QQQNPFCSWMEAHLYQPSLSSLSPGK	330		

SULT 11 -10-408-901-2 Sequence 2, Application US/11408901
 Publication No. US2004023313A1
 GENERAL INFORMATION:
 APPLICANT: Boyle, William
 APPLICANT: Huang, Haichun
 APPLICANT: Elliott, Robin
 APPLICANT: Sullivan, John
 APPLICANT: Medlock, Eugene
 APPLICANT: Martin, Francis
 TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPG Pathway
 TITLE OF INVENTION: Inhibitors
 FILE REFERENCE: MBIB 01-1145-A
 CURRENT APPLICATION NUMBER: US/10/408,901
 CURRENT FILING DATE: 2003-04-07
 NUMBER OF SEQ ID NOS: 76
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 2

RESULT 13
US-10-257-907-5
; Sequence 5, Application US/10257907
; Publication No. US/0040043022A1
; GENERAL INFORMATION:
; APPLICANT: Hauer, Josef
; APPLICANT: Liu, Jingqi
; APPLICANT: Song, Ho Yeong
; APPLICANT: Yang, Derek Di
; TITLE OF INVENTION: TREATING T-CELL MEDIATED DISEASES BY MODULATING DR6 ACTIVITY
; FILE REFERENCE: X-13992
; CURRENT APPLICATION NUMBER: US/10/257,907
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 5
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; SEQ ID NO-257-907-5
; SEQ ID NO: 301 QCGNVSFCSWHEALTHYQORSLSLSPGK 330
; SEQ ID NO: 301 QCGNVSFCSWHEALTHYQORSLSLSPGK 330
; US-10-656-769-2

Query Match 98.0%; Score 1729; DB 15; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.4e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVPLAPSKTCKVSNKALPAPIEKTKAKVOPREPOVYTLPSSRDE 240
Db 1 ASTKGPSVPLAPSKTSGGTTAAAGCLVKDYFPEPVTVWSNGALTSGVHTFPAVLQSS 60
Qy 1 LTKNQSLTCVLYKGFPSDIAVEENGQENNYKTTPVLDGSFFFLYSKLTVDSRWR 300
Db 241 LTKNQSLTCVLYKGFPSDIAVEENGQENNYKTTPVLDGSFFFLYSKLTVDSRWR 300
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; SEQ ID NO-257-907-5
; SEQ ID NO: 301 QCGNVSFCSWHEALTHYQORSLSLSPGK 330
; US-10-656-769-2

Query Match 98.0%; Score 1729; DB 15; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.4e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVPLAPSKTCKVSNKALPAPIEKTKAKVOPREPOVYTLPSSRDE 240
Db 1 ASTKGPSVPLAPSKTSGGTTAAAGCLVKDYFPEPVTVWSNGALTSGVHTFPAVLQSS 60
Qy 1 GLYLSLSVVTVSSSIGTQTYICNWNHKPSNTKVKDKVTEPKSDCITHCPCPAPELLGG 120
Db 61 GLYLSLSVVTVSSSIGTQTYICNWNHKPSNTKVKDKVTEPKSDCITHCPCPAPELLGG 120
Qy 1 PSVFLFPKPKPDTLMISRTPEVTVVVDVSHEDPEEVKNNYVDGTEVHNVKTKPREQYN 180
Db 121 PSVFLFPKPKPDTLMISRTPEVTVVVDVSHEDPEEVKNNYVDGTEVHNVKTKPREQYN 180
Qy 1 STYRVVSLTCLVKGFPYPSDIAVEENGOPENNYKTTPVLDGSFFFLYSKLTVDSRWR 300
Db 181 STYRVVSLTCLVKGFPYPSDIAVEENGOPENNYKTTPVLDGSFFFLYSKLTVDSRWR 300
Qy 1 LTKNQSLTCVLYKGFPSDIAVEENGOPENNYKTTPVLDGSFFFLYSKLTVDSRWR 300
Db 121 LTKNQSLTCVLYKGFPSDIAVEENGOPENNYKTTPVLDGSFFFLYSKLTVDSRWR 300
; CURRENT FILING DATE: 2002-10-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 5
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; SEQ ID NO-257-907-5
; SEQ ID NO: 301 QCGNVSFCSWHEALTHYQORSLSLSPGK 330
; SEQ ID NO: 301 QCGNVSFCSWHEALTHYQORSLSLSPGK 330
; US-10-257-907-5
; Sequence 5, Application US/10257907
; Publication No. US/0040043022A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.,
; APPLICANT: Presnell, Scott R.,
; APPLICANT: Gao, Zeren,
; APPLICANT: Whitmore, Theodore E.,
; APPLICANT: Kuijper, Joseph L.,
; APPLICANT: Maurer, Mark F.,
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/10/772,531
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US/09/892,949
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 38
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens

RESULT 14
US-10-656-769-2
; Sequence 2, Application US/10656769
; Publication No. US/2004/0097712A1
; GENERAL INFORMATION:
; APPLICANT: Varnum, Brian
; APPLICANT: Witte, Alison

-10-772-531-38

Query	Match	Score	DB	Length
Best	Local	98.0%	1729	330
Matches	Similarity	97.9%	Pred. No.	6.4e-126
	Conservative	3 ; Mismatches	4 ;	Indels 0 ; Gaps 0 ;
1	ASTKGPSVFPLAPSKSTS	GGTAALGCLVKDYFPPPTVSWNSGALTSGVHTPVA	LQSS	60
1	ASTKGPSVFPLAPSKSTS	GGTAALGCLVKDYFPPPTVSWNSGALTSGVHTPVA	LQSS	60
61	GLYSLSSTVTVSSISLGQT	YICNWNHKPSNTKUDYKVBBKSCDTH1CPCPAPELIGG	120	
61	GLYSLSSTVTVSSISLGQT	YICNWNHKPSNTKVKDKVEPKSCDTH1CPCPAPELIGG	120	
121	PSVFLFPPKPKDTLMISRTPEVTCVVVDSEHDPEVKWVYDGYEVINVKTPREEQYN	180		
121	PSVFLFPPKPKDTLMISRTPEVTCVVVDSEHDPEVKWVYDGYEVINAKTPREEQYN	180		
181	STYRVSVLTVLHQNNMNGKEYKCKVSNKALPAPIEKTISKAKVPREQVYLP	PSRDE	240	
181	STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGPREQVYLP	PSRDE	240	
241	LTQNOVSLTCLYKGFYPSDIAYEWESNGOPENNYKTPVYLDVGFSFLYSKLTVDSRW	300		
241	LTQNOVSLTCLYKGFYPSDIAYEWESNGOPENNYKTPVYLDSDGSFLYSKLTVDSRW	300		
301	QQGNVFCSCSYMMHEALNNHYQRSLSLSPGK	330		
301	QQGNVFCSCSYMMHEALNNHYTQSLSPGK	330		

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 b time : 102.936 secs

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protein - protein search, using Bw model

on: October 27, 2004, 16:51:34 ; Search time 32.8826 Seconds
 (without alignments)
 665.548 Million cell updates/sec

file: US-10-000-439-2
 Effect score: 1764

quence: 1 ASTKGPSVPLAPSSKSTSG.....MHEALTHHYCORSLSLSPGK 330
 oring table: BLOSUM62

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 arched:

total number of hits satisfying chosen parameters: 478139

minimum DB seq length: 0
 maximum DB seq length: 2000000000

ist-processing: Maximum Match 0%
 Maximum Match 100%

Listing first 45 summaries

atabase :

Issued Patents AA:
 1: /cgn2_6/podata/1/iaa/5A COMB Dep: *
 2: /cgn2_6/podata/1/iaa/5B COMB Dep: *
 3: /cgn2_6/podata/1/iaa/6A COMB Dep: *
 4: /cgn2_6/podata/1/iaa/6B COMB Dep: *
 5: /cgn2_6/podata/1/iaa/PCFTS COMB Dep: *
 6: /cgn2_6/podata/1/iaa/backFiles1.Dep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1729	98.0	371	1	US-08-235-311-7	Sequence 7, Appli
2	1729	98.0	371	3	US-08-457-918-7	Sequence 7, Appli
3	1729	98.0	371	4	US-10-157-408-7	Sequence 7, Appli
4	1729	98.0	446	3	US-08-397-411-7	Sequence 7, Appli
5	1729	98.0	449	1	US-08-455-516-13	Sequence 13, Appli
6	1729	98.0	467	4	US-08-030-175-41	Sequence 42, Appli
7	1729	98.0	467	4	US-08-033-175-42	Sequence 42, Appli
8	1729	98.0	476	2	US-08-370-939-10	Sequence 10, Appli
9	1729	98.0	547	4	US-09-746-352A-54	Sequence 54, Appli
10	1729	98.0	567	4	US-09-825-1561A-16	Sequence 53, Appli
11	1729	98.0	571	4	US-09-746-359A-53	Sequence 53, Appli
12	1729	98.0	951	4	US-09-311-942-9	Sequence 9, Appli
13	1725	97.8	462	4	US-08-289-942A-7	Sequence 7, Appli
14	1725	97.8	475	6	US-08-740-002-27	Sequence 27, Appli
15	1725	97.8	476	3	US-08-487-550-4	Sequence 4, Appli
16	1725	97.8	476	3	US-08-487-550-12	Sequence 12, Appli
17	1725	97.8	476	4	US-08-526-098-4	Sequence 4, Appli
18	1725	97.8	476	4	US-08-526-098-12	Sequence 12, Appli
19	1725	97.8	476	4	US-09-383-916-4	Sequence 4, Appli
20	1725	97.8	476	4	US-08-383-916-12	Sequence 12, Appli
21	1725	97.8	478	3	US-08-487-550-8	Sequence 8, Appli
22	1725	97.8	478	4	US-08-526-098-8	Sequence 8, Appli
23	1724	97.7	478	4	US-08-383-916-8	Sequence 7, Appli
24	1724	97.7	459	1	US-08-157-101A-7	Sequence 25, Appli
25	1724	97.7	475	4	US-08-740-002-25	Sequence 22, Appli
26	1723	97.7	330	4	US-09-301-593-22	Sequence 14, Appli
27	1723	97.7	451	2	US-08-887-352B-14	Sequence 2, Appli

RESULT 1

US-08-236-311-7

Sequence 7, Application US/08236311

Patent No. 5565335

GENERAL INFORMATION

Applicant: Capon, Daniel J.

Applicant: Gregory, Timothy J.

Title of Invention: Adheson variants

Number of Sequences: 25

CORRESPONDENCE ADDRESS:

Address: Genentech, Inc.

Street: 460 Point San Bruno Blvd

City: South San Francisco

State: California

Country: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM: 5.25 inch, 360 Kb floppy disk

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Patin (Genentech)

CURRENT APPLICATION DATA:

Application Number: US/08/236,311

Filing Date: 02-MAY-1994

Prior Application Data:

Application Number: 07/936190

Filing Date: 26-AUG-1992

Prior Application Data:

Application Number: 07/8422777

Filing Date: 18-FEB-1992

Prior Application Data:

Application Number: 07/250785

Filing Date: 28-SEP-1988

Prior Application Data:

Application Number: 07/104329

Filing Date: 02-OCT-1987

Attorney/Agent Information:

Name: Hasak, Janet E.

Registration Number: 28,616

Reference Docket Number: 444P1C2

Telecommunication Information:

Telephone: 415/952-1896

Telex: 910/371-7168

Information: SEQ ID NO: 7;

SEQUENCE CHARACTERISTICS:

Length: 25,

Type: 371 amino acids

Topology: linear

ALIGNMENTS

US-08-236-311-7

Query Match 98.0%; Score 1729; DB 1; Length 371;
Best Local Similarity 97.9%; Pred. No. 3e-157; Indels 0; Gaps 0;
Matches 323; Conservative 3; Mismatches 4; Insertions 0; Gaps 0;

Qy 1 ASTKGPSVYPLAPSSKSTSGGTAALCCLVQRDYYFPEPVTVWSNSGALTSGVHTFPAVLQSS 60
Db 42 ASTKGPSVYPLAPSSKSTSGGTAALCCLVQRDYYFPEPVTVWSNSGALTSGVHTFPAVLQSS 101

Qy 61 GLYSLSVVTVYPTBSSSLGTQTYICNTHKPSNTKVDKVEPKSCDKTKHCPCPBPAPLIGG 120
Db 102 GLYSLSVVTVYPTBSSSLGTQTYICNTHKPSNTKVDKVEPKSCDKTKHCPCPBPAPLIGG 161

Qy 121 PSVFLFPKPKDTLMISRTPETVTVYDVSHEDEPEVKENWYDGVEVANVKTPREEQYN 180
Db 162 PSVFLFPKPKDTLMISRTPETVTVYDVSHEDEPEVKENWYDGVEVANAKTKTPREEQYN 221

Qy 181 STYRVSVLTIVHQDWINGKEYKCVSNKALPAPLKTISKAVQPREQVTLPPRDE 240
Db 222 STYRVSVLTIVHQDWINGKEYKCVSNKALPAPLKTISKAGQPREQVTLPPRDE 281

Qy 241 LTKNOVSLTCLVKGFYPSDIAVEWESNGQPNENYKTTPVLDVGSSFLYSLSKLTVDKSRW 300
Db 282 LTKNOVSLTCLVKGFYPSDIAVEWESNGQPNENYKTTPVLDVGSSFLYSLSKLTVDKSRW 341

Qy 301 QGGNVFSCSYVMHEALHYCORSLSLSPGK 330
Db 342 QGGNVFSCSYVMHEALHYCORSLSLSPGK 371

RESULT 2

US-08-236-311-7

; Parent NO. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIAN TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,918
FILING DATE: 1-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/236311
FILING DATE: 02-MAY-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.

REGISTRATION NUMBER: 36-575
REFERENCE/DOCKET NUMBER: P0444PIC3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9841
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-457-918-7

Query Match 98.0%; Score 1729; DB 3; Length 371;
Best Local Similarity 97.9%; Pred. No. 3e-157; Indels 0; Gaps 0;
Matches 323; Conservative 3; Mismatches 4; Insertions 0; Gaps 0;

Qy 1 ASTKGPSVYPLAPSSKSTSGGTAALCCLVQRDYYFPEPVTVWSNSGALTSGVHTFPAVLQSS 60
Db 42 ASTKGPSVYPLAPSSKSTSGGTAALCCLVQRDYYFPEPVTVWSNSGALTSGVHTFPAVLQSS 101

Qy 61 GLYSLSVVTVYPTBSSSLGTQTYICNTHKPSNTKVDKVEPKSCDKTKHCPCPBPAPLIGG 120
Db 102 GLYSLSVVTVYPTBSSSLGTQTYICNTHKPSNTKVDKVEPKSCDKTKHCPCPBPAPLIGG 161

Qy 121 PSVFLFPKPKDTLMISRTPETVTVYDVSHEDEPEVKENWYDGVEVANVKTPREEQYN 180
Db 162 PSVFLFPKPKDTLMISRTPETVTVYDVSHEDEPEVKENWYDGVEVANAKTKTPREEQYN 221

Qy 181 STYRVSVLTIVHQDWINGKEYKCVSNKALPAPLKTISKAVQPREQVTLPPRDE 240
Db 222 STYRVSVLTIVHQDWINGKEYKCVSNKALPAPLKTISKAGQPREQVTLPPRDE 281

Qy 241 LTKNOVSLTCLVKGFYPSDIAVEWESNGQPNENYKTTPVLDVGSSFLYSLSKLTVDKSRW 300
Db 282 LTKNOVSLTCLVKGFYPSDIAVEWESNGQPNENYKTTPVLDVGSSFLYSLSKLTVDKSRW 341

Qy 301 QGGNVFSCSYVMHEALHYCORSLSLSPGK 330
Db 342 QGGNVFSCSYVMHEALHYCORSLSLSPGK 371

RESULT 3

US-10-157-408-7

; Sequence 7, Application US/10157408
; Patent No. 6710169

GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,918
FILING DATE: 1-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/236311
FILING DATE: 02-MAY-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.

TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/157,408
FILING DATE: 28-May-2002
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/457,918
FILING DATE: 1-JUN-1995
APPLICATION NUMBER: 08/236311
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988

FILING DATE: 26-AUG-1992
 APPLICATION NUMBER: 07/842777
 FILING DATE: 18-FEB-1992
 APPLICATION NUMBER: 07/250785
 FILING DATE: 28-SEP-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Kubinec, Jeffrey S.
 REGISTRATION NUMBER: 36,575
 REFERENCE/DOCKET NUMBER: P4444PLC3
 TELEPHONE: 415/225-8228
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 371 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 :-10-157-408-7:

Query Match	98.0%	Score 1729;	DB 4;	Length 371;	
Best Local Similarity	97.9%	Pred. No. 3e-157;			
Matches	323;	Conservative	3;	Mismatches	0;
1	ASTKGPSVPLASKTSNSGGTAALGLCIVDXFPEPTVSINNSGALTSGYHTFPAPVLOSS	60			
42	ASTKGPSVPLASKTSNSGGTAALGLCIVDXFPEPTVSINNSGALTSGYHTFPAPVLOSS	101			
61	GLYLSLSSVTVTPSSSLGQTQYICNWNHCKPSNTKVDKKEPKSCDKTHTCPCPAPELLGG	120			
102	GLYLSLSSVTVTPSSSLGQTQYICNWNHCKPSNTKVDKKEPKSCDKTHTCPCPAPELLGG	161			
121	PSVFLFPKPKDTMISRTPEYTCAVYDVSHEDPEVKENWYDGVHVNKTKEEQYN	180			
162	PSVFLFPKPKDTMISRTPEYTCAVYDVSHEDPEVKENWYDGVHVNKTKEEQYN	221			
181	STYRVSVTTLVHQWVNGKEYKCVSNKALPAPIEKTISAKVQPREPVYTLPPSRDE	240			
222	STYRVSVTTLVHQWVNGKEYKCVSNKALPAPIEKTISAKVQPREPVYTLPPSRDE	281			
241	LTKNQVSLTCVKGYPSPDIAYEWNSQOPENNYKTTPPVLDGSFFLYSKLTVDKSRW	300			
282	LTKNQVSLTCVKGYPSPDIAYEWNSQOPENNYKTTPPVLDGSFFLYSKLTVDKSRW	341			
301	QQGNVFSCSVMEAHLNHYQORSLSLSPGK	330			
342	QQGNVFSCSVMEAHLNHYTQKSLSLSPGK	371			

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1400LT

1401LT

1402LT

1403LT

1404LT

140

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 SOFTWARE: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/458,516
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/059,159
 FILING DATE: 03-MAY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 11823-37-3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 449 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-458-516-13

Query Match 98.0%; Score 1729; DB 1; Length 449;
 Best Local Similarity 97.9%; Pred. No. 4-e-157;
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVYPLAPSSKSTSGCTAAGCLYDFFPEPVTVSNWSGALTSGVHTFPAVISQSS 60
 Db 120 ASTKGPSVYPLAPSSKSTSGCTAAGCLYDFFPEPVTVSNWSGALTSGVHTFPAVISQSS 179
 Qy 61 GLYSSLSSVTVTYPSSSTGQTQTYICNVNTHKPNTNYDKRVEPKSCDKTHCPCPAPELGG 120
 Db 180 GLYSSLSSVTVTYPSSSTGQTQTYICNVNTHKPNTNYDKRVEPKSCDKTHCPCPAPELGG 239
 Qy 121 PSVFLPPPKPKDTLMISRPTPEVTVYDVSHEDEPKFKNMYVDGEVENVTKTPREEQYN 180
 Db 240 PSVFLPPPKPKDTLMISRPTPEVTVYDVSHEDEPKFKNMYVDGEVENVNAKTPREEQYN 299
 Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPVQYTLPPRDE 240
 Db 300 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPVQYTLPPRDE 359
 Qy 241 LTKNOVSLTCLVKGFPSDIAVEWNSQOPENNYKTPVLDGSFLYSLXLTVDKSRW 300
 Db 360 LTKNOVSLTCLVKGFPSDIAVEWNSQOPENNYKTPVLDGSFLYSLXLTVDKSRW 419
 Qy 301 QQQNVSFCSCSYMEALHNYHQRSLSLSPGK 330
 Db 420 QQQNVSFCSCSYMEALHNYHQRSLSLSPGK 449

RESULT 6
 US-08-030-175-41
 ; Sequence 41, Application US/08030175
 ; GENERAL INFORMATION:
 ; APPLICANT: Gorman, Scott D.
 ; APPLICANT: Clark, Michael R.
 ; APPLICANT: Cobbold, Stephen P.
 ; APPLICANT: Waldmann, Herman
 ; TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION
 ; NUMBER OF SEQUENCES: 43
 ; CORRESPONDENCE ADDRESS:
 ; STREET: 555 13TH ST., NW Suite 701 East
 ; CITY: Washington
 ; STATE: D. C.
 ; COUNTRY: U.S.

RESULT 7
 US-08-030-175-42
 ; Sequence 42, Application US/08030175
 ; GENERAL INFORMATION:
 ; APPLICANT: Gorman, Scott D.
 ; APPLICANT: Clark, Michael R.
 ; APPLICANT: Cobbold, Stephen P.
 ; APPLICANT: Waldmann, Herman
 ; TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION
 ; NUMBER OF SEQUENCES: 43
 ; CORRESPONDENCE ADDRESS:
 ; STREET: 555 13TH ST., NW Suite 701 East
 ; CITY: Washington
 ; STATE: D. C.
 ; COUNTRY: U.S.

COUNTRY: U.S.
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage
 COMPUTER: IBM AT compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2
 SOFTWARE: WordPerfect 5.0 (DOS Text)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/030,175
 FILING DATE: 17-MAY-1993
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB91/01578
 FILING DATE: 13-SEP-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: ERNST, Barbara G.
 REGISTRATION NUMBER: 30,377
 REFERENCE/DOCKET NUMBER: 1768-118
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 783-6040
 TELEFAX: (202) 783-6031
 INFORMATION FOR SEQ ID NO: 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 467 amino acids
 /TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 -08-030-175-42

Query Match 98.0%; Score 1729; DB 4; Length 467;
 Best Local Similarity 97.9%; Pred. No. 4.2e-157;
 Matches 323; Conservative 3; Mismatches 0; Gaps 0;

1	ASTKGPSVPLAPSXSKTSGTTAALGLVQDYFPEPYTVSNNSGALTSGYHTFPAVLOSS	60
138	ASTKGPSVPLAPSXSKTSGTTAALGLVQDYFPEPYTVSNNSGALTSGYHTFPAVLOSS	197
61	GLYLSSSVVTVPSLGTQTYCNVHRPSNTKVDKVEPKSCDKTHTCPCPAPELGG	120
198	GLYLSSSVVTVPSLGTQTYCNVHRPSNTKVDKVEPKSCDKTHTCPCPAPELGG	257
121	PSVFLPPKPKDLMISRTPEYCFVNYYDGVFVNKTKEEQYN	180
258	PSVFLPPKPKDLMISRTPEYCFVNYYDGVFVNKTKEEQYN	317
181	STYRVSVLTVHQNWNGKEYKCKVSNKALPAPLEKTIKAKVQPREFQYTLPPSDE	240
318	STYRVSVLTVHQDWLNGKEYKCKVSNKALPAPLEKTIKAKVQPREFQYTLPPSDE	377
241	LTKNQVSLLTCLVKGYFPSDIATEWSNGOPENNYKTPPVLDGSFFLYSKLTVDKSRW	300
378	LTKNQVSLLTCLVKGYFPSDIATEWSNGOPENNYKTPPVLDGSFFLYSKLTVDKSRW	437
301	QQGNVFSCSVMHEALHNHYQQESLSSLSPGK	330
438	QQGNVFSCSVMHEALHNHYQQESLSSLSPGK	467

Query Match 98.0%; Score 1729; DB 2; Length 476;
 Best Local Similarity 97.9%; Pred. No. 4.3e-157;
 Matches 323; Conservative 3; Mismatches 0; Gaps 0;
 Qy 1 ASTKGPSVPLAPSXSKTSGTTAALGLVQDYFPEPYTVSNNSGALTSGYHTFPAVLOSS 60
 Db 147 ASTKGPSVPLAPSXSKTSGTTAALGLVQDYFPEPYTVSNNSGALTSGYHTFPAVLOSS 206
 Qy 61 GLYLSSSVVTVPSLGTQTYCNVHRPSNTKVDKVEPKSCDKTHTCPCPAPELGG 120
 Db 207 GLYLSSSVVTVPSLGTQTYCNVHRPSNTKVDKVEPKSCDKTHTCPCPAPELGG 266
 Qy 121 PSVFLPPKPKDLMISRTPEYCFVNYYDGVFVNKTKEEQYN 180 |

SHEDDEVKEMWVYDGVFVNKTKEEQYN

 Db 267 PSVFLPPKPKDLMISRTPEYCFVNYYDGVFVNKTKEEQYN 326
 Qy 181 STYRVSVLTVHQNWNGKEYKCKVSNKALPAPLEKTIKAKVQPREFQYTLPPSDE 240
 Db 327 STYRVSVLTVHQDWLNGKEYKCKVSNKALPAPLEKTIKAKVQPREFQYTLPPSDE 366
 Qy 241 LTKNQVSLLTCLVKGYFPSDIATEWSNGOPENNYKTPPVLDGSFFLYSKLTVDKSRW 300
 Db 387 LTKNQVSLLTCLVKGYFPSDIATEWSNGOPENNYKTPPVLDGSFFLYSKLTVDKSRW 446
 Qy 301 QQGNVFSCSVMHEALHNHYQQESLSSLSPGK 330
 Db 447 QQGNVFSCSVMHEALHNHYQQESLSSLSPGK 476

RESULT 9
 US 09-1746-359A-54
 Sequence 54, Application US/09746359A
 Patent No. 6610286
 GENERAL INFORMATION:
 APPLICANT: CROWE, JAMES SCOTT
 APPLICANT: LEWIS, ALAN PETER
 TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
 NUMBER OF SEQUENCES: 46
 CORRESPONDENCE ADDRESS:
 STREET: 555 THIRTEENTH ST. N.W.
 CITY: WASHINGTON
 STATE: D. C.
 COUNTRY: U.S.

TITLE OF INVENTION: Method for Treating Inflammation

FILE REFERENCE: 99-108
 CURRENT APPLICATION NUMBER: US/09/746,359A
 CURRENT FILING DATE: 2001-05-21
 PRIORITY NUMBER: 60/171,969
 PRIORITY FILING DATE: 1999-12-23
 PRIORITY APPLICATION NUMBER: 60/213,341
 PRIORITY FILING DATE: 2000-06-22
 NUMBER OF SEQ ID NOS: 72
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 54
 LENGTH: 547
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-746-359A-54

Query Match 98.0%; Score 1729; DB 4; Length 567;
 Best Local Similarity 97.9%; Pred. No. 5 6e-157;
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVPLAPSXSTSGCTAAALGLVQDXYFPEPVTVSNSGALTSGVHTFPVALQSS 60
 Db 238 ASTKGPSVPLAPSXSTSGCTAAALGLVQDXYFPEPVTVSNSGALTSGVHTFPVALQSS 297

Qy 61 GLYSLSVVTVSSSLGTTQTYICNNNHPSPNTKVDKKVKEBKSCDKTHTCPCCPAPELGG 120
 Db 298 GLYSLSVVTVSSSLGTTQTYICNNNHPSPNTKVDKKVKEBKSCDKTHTCPCCPAPELGG 357

Qy 121 PSVFLFPKPKDTLMISRPTPEVTVVDDVSHEDEPVKFWYVOGEVHNVKTKRPREQYN 180
 Db 358 PSVFLFPKPKDTLMISRPTPEVTVVDDVSHEDEPVKFWYVOGEVHNVKTKRPREQYN 417

Qy 181 STYRVSVLTVLHQWNLNGKEYKCKVSKNALPAPEKTIKAKVQPREPOVYTLPPSRSDE 240
 Db 418 STYRVSVLTVLHQDWLNGKEYKCKVSKNALPAPEKTIKAKGQPREQVYTLPPSRSDE 477

Qy 218 ASTKGPSVPLAPSXSTSGCTAAALGLVQDXYFPEPVTVSNSGALTSGVHTFPVALQSS 277

Qy 61 GLYSLSVVTVSSSLGTTQTYICNNNHPSPNTKVDKKVKEBKSCDKTHTCPCCPAPELGG 120
 Db 278 GLYSLSVVTVSSSLGTTQTYICNNNHPSPNTKVDKKVKEBKSCDKTHTCPCCPAPELGG 337

Qy 121 PSVFLFPKPKDTLMISRPTPEVTVVDDVSHEDEPVKFWYVOGEVHNVKTKRPREQYN 180
 Db 338 PSVFLFPKPKDTLMISRPTPEVTVVDDVSHEDEPVKFWYVOGEVHNVKTKRPREQYN 397

RESULT 11 US-09-746-359A-53

Qy 181 STYRVSVLTVLHQWNLNGKEYKCKVSKNALPAPEKTIKAKVQPREPOVYTLPPSRSDE 240
 Db 398 STYRVSVLTVLHQDWLNGKEYKCKVSKNALPAPEKTIKAKGQPREQVYTLPPSRSDE 457

Qy 241 LTKNQSLTCLVKGFYPSDAVEWESNGOPENNYKTPPVLDVSFGFLYSLKLTVDKSRW 300
 Db 458 LTKNQSLTCLVKGFYPSDAVEWESNGOPENNYKTPPVLDSDGSTFPLYSLKLTVDKSRW 517

Qy 301 QGGNFSCSYNHEALTHYHHCORSLSLSPGK 330
 Db 518 QGGNFSCSYNHEALTHYHHCORSLSLSPGK 547

RESULT 10 US-09-825-561A-16

Sequence 16, Application US/09825561A

GENERAL INFORMATION:
 / APPLICANT: Sprecher, Cindy A.
 / APPLICANT: West, James W.
 / APPLICANT: Presnell, Scott R.
 / APPLICANT: Holly, Richard D.
 / APPLICANT: Nelson, Andrew J.
 / TITLE OF INVENTION: SOLUBLE ZALPHAI1 CYTOKINE RECEPTORS
 / FILE REFERENCE: 00-222
 / CURRENT APPLICATION NUMBER: US/09/825,561A
 / CURRENT FILING DATE: 2000-04-05
 / PRIORITY NUMBER: US 60/194;731
 / PRIOR FILING DATE: 2000-04-05
 / PRIOR APPLICATION NUMBER: US 60/222,121
 / PRIOR FILING DATE: 2000-07-28
 / NUMBER OF SEQ ID NOS: 86
 / SOFTWARE: FastSEQ for Windows Version 3.0
 / SEQ ID NO: 16
 / LENGTH: 567
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE: OTHER INFORMATION: soluble zalpha1I/IGGammal polypeptide
 / US-09-825-561A-16

Query Match 98.0%; Score 1729; DB 4; Length 571;
 Best Local Similarity 97.9%; Pred. No. 5 7e-157;
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVPLAPSXSTSGCTAAALGLVQDXYFPEPVTVSNSGALTSGVHTFPVALQSS 60
 Db 242 ASTKGPSVPLAPSXSTSGCTAAALGLVQDXYFPEPVTVSNSGALTSGVHTFPVALQSS 301

Qy 61 GLYSLSVVTVSSSLGTTQTYICNNNHPSPNTKVDKKVKEBKSCDKTHTCPCCPAPELGG 120
 Db 302 GLYSLSVVTVSSSLGTTQTYICNNNHPSPNTKVDKKVKEBKSCDKTHTCPCCPAPELGG 361

121 PSVFLFPKPKDTLMSRTPETVTCVVYDVSHEDEPEVKPNWYDGVEVHNVTKPREEQYN 180
 362 PSVLFPPKPKDTLMSRTPETVCCVVYDVSHEDEPEVKPNWYDGVEVHNVTKPREEQYN 421

181 STYRVSVLTILHQNWNGKEYKCRYSNKAAPAKTISAKAVOPREPOVYTLPSRDE 240
 422 STYRVSVLTILHQDWLNGKEYKCVSNKAALPAPAKTISAKGQPREPOVYTLPSRDE 481

241 LTKQVSLTCLVKGFYPSDIATEWSNGOPENNYKTTPVLDSSFFLYSKLTVDKSRW 300
 482 LTKQVSLTCLVKGFYPSDIATEWSNGOPENNYKTTPVLDSSFFLYSKLTVDKSRW 541

301 QGNVFSCSYMHAEALHHYQQRSLSSLSPGK 330
 542 QGNVFSCSYMHAEALHHYQTSSLSPGK 571

542 QGNVFSCSYMHAEALHHYQTSSLSPGK 571

)SULT 112
 ->09-313-942-9
 Sequence 9, Application US/09313942
 Patent No. 6472179
 GENERAL INFORMATION:
 APPLICANT: PHARMACEUTICALS, INC.
 TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
 TITLE OF INVENTION: AND USING
 FILE REFERENCE: REG 203-A
 CURRENT FILING DATE: 1999-05-19
 PRIOR FILING DATE: 1999-05-19
 PRIOR APPLICATION NUMBER: 60/101,858
 PRIOR FILING DATE: 1998-09-25
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 9
 LENGTH: 951
 TYPE: PRT
 ORGANISM: Homo sapiens
)->09-313-942-9

Query Match 98.0%; Score 1729; DB 4; Length 951;
 Best Local Similarity 97.9%; Pred. No. 1.2e-156;
 Matches 323; Conservative 3; Mismatches 14; Indels 0; Gaps 0;
 SEQ ID NO 9
 LENGTH: 951
 TYPE: PRT
 ORGANISM: Homo sapiens
)->09-313-942-9

1 ASTRGPSVPLASKSPTSGGTAAALGLIVKDFPPEPTVWSNSGALTSGVHTPPVLOSS 60
 622 ASTRGPSVPLASKSPTSGGTAAALGLIVKDFPPEPTVWSNSGALTSGVHTPPVLOSS 681

61 GLYSLSVVTVPSPLSSGLTQTYICNNVHKPSNTKVDKKEPKSCDKTHCPCPAPELGG 120
 682 GLYSLSVVTVPSPLSSGLTQTYICNNVHKPSNTKVDKKEPKSCDKTHCPCPAPELGG 741

1 ASTRGPSVPLASKSPTSGGTAAALGLIVKDFPPEPTVWSNSGALTSGVHTPPVLOSS 60
 622 ASTRGPSVPLASKSPTSGGTAAALGLIVKDFPPEPTVWSNSGALTSGVHTPPVLOSS 681
 61 GLYSLSVVTVPSPLSSGLTQTYICNNVHKPSNTKVDKKEPKSCDKTHCPCPAPELGG 120
 682 GLYSLSVVTVPSPLSSGLTQTYICNNVHKPSNTKVDKKEPKSCDKTHCPCPAPELGG 741

121 PSVFLFPKPKDTLMSRTPETVTCVVYDVSHEDEPEVKPNWYDGVEVHNVTKPREEQYN 180
 742 PSVLFPPKPKDTLMSRTPETVCCVVYDVSHEDEPEVKPNWYDGVEVHNVTKPREEQYN 801

181 STYRVSVLTILHQNWNGKEYKCVSNKAAPAKTISAKAVOPREPOVYTLPSRDE 240
 802 STYRVSVLTILHQDWLNGKEYKCVSNKAALPAPAKTISAKGQPREPOVYTLPSRDE 861

241 LTKQVSLTCLVKGFYPSDIATEWSNGOPENNYKTTPVLDSSFFLYSKLTVDKSRW 300
 862 LTKQVSLTCLVKGFYPSDIATEWSNGOPENNYKTTPVLDSSFFLYSKLTVDKSRW 921

301 QGNVFSCSYMHAEALHHYQQRSLSSLSPGK 330
 922 QGNVFSCSYMHAEALHHYQTSSLSPGK 951

)SULT 13
 3-09-289-942A-7
 Sequence 7, Application US/09289942A

;) Patent No. 6462928
 ; GENERAL INFORMATION:
 ; APPLICANT: Pai, Emil F.
 ; APPLICANT: Chong, Pele H.
 ; APPLICANT: Edyczak, Arthur
 ; TITLE OF INVENTION: Fab, -EPITOPE COMPLEX FROM THE HIV-1 CROSS-NEUTRALIZING MONOCLONAL ANTIBODY 2F5
 ; FILE REFERENCE: 1038-926 MLS:jb
 ; CURRENT APPLICATION NUMBER: US/09/289, 942A
 ; CURRENT FILING DATE: 1999-04-13
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 462
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus type 1
 ; US-09-289-942A-7

Query Match 97.8%; Score 1725; DB 4; Length 462;
 Best Local Similarity 97.6%; Pred. No. 1e-156;
 Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ASTKGPSVPLASKSPTSGGTAAALGLIVKDFPPEPTVWSNSGALTSGVHTPPVLOSS 60
 Db 133 ASTKGPSVPLASKSPTSGGTAAALGLIVKDFPPEPTVWSNSGALTSGVHTPPVLOSS 192

Qy 61 GLYSLSVVTVPSPLSSGLTQTYICNNVHKPSNTKVDKKEPKSCDKTHCPCPAPELGG 120
 Db 193 GLYSLSVVTVPSPLSSGLTQTYICNNVHKPSNTKVDKKEPKSCDKTHCPCPAPELGG 252

Qy 121 PSVFLFPKPKDTLMSRTPETVTCVVYDVSHEDEPEVKENWYVQGVEVHNVTKPREEQYN 180
 Db 253 PSVFLFPKPKDTLMSRTPETVTCVVYDVSHEDEPEVKENWYVQGVEVHNVTKPREEQYN 312

Qy 181 STYRVSVLTILHQNWNGKEYKCVSNKAALPAPAKTISAKAVOPREPOVYTLPSRDE 240
 Db 313 STYRVSVLTILHQDWLNGKEYKCVSNKAALPAPAKTISAKAVOPREPOVYTLPSRDE 372

Qy 241 LTKQVSLTCLVKGFYPSDIATEWSNGOPENNYKTTPVLDSSFFLYSKLTVDKSRW 300
 Db 373 LTKQVSLTCLVKGFYPSDIATEWSNGOPENNYKTTPVLDSSFFLYSKLTVDKSRW 433

RESULT 14
 US-09-740-002-27
 Sequence 27, Application US/09740002
 ; Patent No. 657809
 ; GENERAL INFORMATION:
 ; APPLICANT: BRAMS, PETER
 ; APPLICANT: MORROW, PHILLIP
 ; TITLE OF INVENTION: HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
 ; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
 ; TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
 ; FILE REFERENCE: 037003-0275759
 ; CURRENT APPLICATION NUMBER: US/09/740, 002
 ; CURRENT FILING DATE: 2000-12-20
 ; PRIOR APPLICATION NUMBER: 09/335, 697
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 08/488, 376
 ; PRIOR FILING DATE: 1995-06-07
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 27
 ; LENGTH: 75
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-740-002-27

Query Match 97.8%; Score 1725; DB 4; Length 475;
 Best Local Similarity 97.6%; Pred. No. 1e-156; 3; Mismatches
 Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ASTKGPSVPLAPSRSKTSGGTAALGLVRYFPBPVTVNSGALTSGVHTFPAVLOSS 60
 Db 146 ASTKGPSVPLAPSRSKTSGGTAALGLVRYFPBPVTVNSGALTSGVHTFPAVLOSS 205

Qy 61 GLYSSLSSVTVTPSSIGTQTYICNVNHRPKBPNTRDVKVEPKSCDKTHCPCPAPELGG 120
 Db 206 GLYSSLSSVTVTPSSIGTQTYICNVNHRPKBPNTRDVKVEPKSCDKTHCPCPAPELGG 265

Qy 121 PSVFLPPKPKDLMISRTPEVTCVWVDSHEDPVKFNWYDGVEVHNKTPREEQYN 180
 Db 266 PSVFLPPKPKDLMISRTPEVTCVWVDSHEDPVKFNWYDGVEVHNKTPREEQYN 325

Qy 181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVTLPGRDE 240
 Db 326 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVTLPGRDE 385

Qy 241 LTKNOVSITCLVKFYSKPSDIAVEWESNGQPENNYKTPVLDVSKLTVDKSRW 300
 Db 386 LTKNOVSITCLVKFYSKPSDIAVEWESNGQPENNYKTPVLDVSKLTVDKSRW 445

Qy 301 QQGNVFSCSVMEHALNHYQQSLSLSPGK 330
 Db 446 QQGNVFSCSVMEHALNHYQQSLSLSPGK 476

RESULT 15
 US-08-487-550-4
 ; Sequence 4, Application US/08487550
 ; Patent No. 6113898

RESULT 15
 US-08-487-550-4

; Sequence 4, Application US/08487550

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONOCLONAL ANTIBODIES SPECIFIC

; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.3.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,550

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 476 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-487-550-4

Query Match 97.8%; Score 1725; DB 3; Length 476;
 Best Local Similarity 97.6%; Pred. No. 1e-156;

Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 ASTKGPSVPLAPSRSKTSGGTAALGLVRYFPBPVTVNSGALTSGVHTFPAVLOSS 60
 Db 147 ASTKGPSVPLAPSRSKTSGGTAALGLVRYFPBPVTVNSGALTSGVHTFPAVLOSS 205

Qy 61 GLYSSLSSVTVTPSSIGTQTYICNVNHRPKBPNTRDVKVEPKSCDKTHCPCPAPELGG 120
 Db 207 GLYSSLSSVTVTPSSIGTQTYICNVNHRPKBPNTRDVKVEPKSCDKTHCPCPAPELGG 266

Qy 121 PSVFLPPKPKDLMISRTPEVTCVWVDSHEDPVKFNWYDGVEVHNKTPREEQYN 180
 Db 267 PSVFLPPKPKDLMISRTPEVTCVWVDSHEDPVKFNWYDGVEVHNKTPREEQYN 326

Db 181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVTLPGRDE 240
 Db 327 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGPREPQVTLPGRDE 386

Db 241 LTKNOVSITCLVKFYSKPSDIAVEWESNGQPENNYKTPVLDVSKLTVDKSRW 300

Db 387 LTKNOVSITCLVKFYSKPSDIAVEWESNGQPENNYKTPVLDVSKLTVDKSRW 446

Qy 301 QQGNVFSCSVMEHALNHYQQSLSLSPGK 330
 Db 447 QQGNVFSCSVMEHALNHYQQSLSLSPGK 476

Search completed: October 27, 2004, 17:05:52
 Job time : 34.8826 secs

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4 protein - Protein search, using sw model

on: October 27, 2004, 16:51:09 ; Search time 20:22:78 Seconds
 (without alignments)
 1101.547 Million cell updates/sec

title: US-10-000-439-3
 effect score: 1460
 sequence: 1 EPKSCDXTHTCPPCPAPELIL.....MHEALINHYQRSLSLSPGK 232
 scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database :

BIR_79:*
 1: Pir1:
 2: Pir2:
 3: Pir3:
 4: Pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1225	97.2	330	1	GHHU	Ig Gamma-1 chain C
2	1219	97.2	374	2	S6933_9	Ig heavy chain V _r
3	1217	96.6	255	4	S3186_4	Ig gamma-1 chain C
4	1172	93.0	234	2	PT007	Ig Gamma-3 chain C
5	1138	90.3	377	2	A23511	Ig Gamma-3 chain C
6	1136	90.2	377	2	A6076_4	Ig Gamma-3 chain C
7	1123	89.1	289	1	G3HWI	Ig Gamma-3 chain C
8	1107	87.9	326	1	G2HU	Ig Gamma-2 chain C
9	1097	87.1	327	1	G4HU	Ig Gamma-2 chain C
10	883	70.1	323	1	GHRB	Ig Gamma-2 chain C
11	868.5	68.9	328	2	I4716_0	Ig Gamma-2 chain C
12	868.5	68.9	328	2	I4711_9	Ig Gamma-2 chain C
13	865	68.7	277	2	I4716_2	Ig Gamma-4 chain C
14	858	68.1	329	2	G2GP	Ig Gamma-2 chain C
15	847.5	67.3	328	2	I4715_8	Ig Gamma-1 chain C
16	840.5	66.7	328	2	I4716_1	Ig Gamma-3 chain C
17	820	65.1	470	2	S22010	Ig heavy chain Pre
18	813	64.5	333	2	PS0018	Ig Gamma-2b chain
19	812.5	64.5	329	1	G3MSMC	Ig Gamma-3 chain C
20	811.5	64.4	308	2	C3054	Ig heavy chain C
21	811.5	64.4	472	2	S3159	Ig Gamma-1 chain C
22	801.5	63.6	398	1	G3MSM	Ig Gamma-3 chain C
23	794.5	63.1	444	2	PC443_6	monoclonal antibody
24	789.5	62.7	324	1	G1MS	Ig Gamma-1 chain C
25	784.5	62.3	326	2	PS0017	Ig Gamma-1 chain C
26	784.5	62.3	393	1	G1MSM	Ig Gamma-1 chain C
27	776.5	51.6	329	2	S00847	Ig Gamma-2c chain
28	776	61.6	330	1	G2MSA	Ig Gamma-2a chain
29	776	61.6	469	2	S37433	Ig Gamma-2a chain

RESULT 1

GHHU

Ig gamma-1 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004

C;Accession: A93433; S36881; S33887; B90611; A90564; B91668; A91723; A02146

R;Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 401-409, 1982

A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A;Reference number: A93433; MUID:82274238; PMID:6287432

A;Accession: A93433

A;Molecule type: DNA

A;Residues: 1-330 <ELL>

A;Cross references: UNIPROT:PO1857; EMBL:217370

A;Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) markers, 2

A;Note: Lys-330 is removed after translation

R;Harris, L.J.

submitted to the EMBL Data Library, October 1992

A;Reference number: S33904

A;Accession: S36561

A;Molecule type: DNA

A;Residues: 2-330 <HR>

A;Cross references: EMBL:217370

R;Takahashi, N.; Ueda, S.; Obara, M.; Nikaido, T.; Nakai, S.; Honjo, S.

Cell 29, 671-679, 1982

A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a c

A;Reference number: S33887; MUID:83001943; PMID:6811139

A;Accession: S33887

A;Molecule type: DNA

A;Residues: 88-113; 235-330 <TAK>

A;Cross references: EMBL:217370

R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Maxdal, M.J.; Edelman, C

Biochemistry 9, 3161-3170, 1970

A;Title: The covalent structure of a human gammag-immunoglobulin. VII. Amino acid sequenc

A;Reference number: A90564; MUID:71064024; PMID:5489771

A;Contents: myeloma protein Eu

A;Accession: B90563

A;Molecule type: Protein

A;Residues: 1-96, R, 98-115 <CUN>

A;Note: this sequence has the Glm(3) marker, 97-Arg

R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A;Title: The covalent structure of a human gammag-immunoglobulin. VIII. Amino acid sequenc

A;Reference number: A90564; MUID:71064025; PMID:5530842

A;Contents: Eu

A;Accession: A90564

A;Molecule type: Protein

A;Residues: 136-154, Q, 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240, '

R;Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A;Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

igen Primaerstruktur.

A;Reference number: A91668; MUID: 77070269; PMID: 826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34; 'Q', '36-96', 'K', '98-117', 'Q', '117-197', 'D', '199-238', 'D', '242-268', 'E', '27
A;Note: this sequence has the Gim(1) and Gim(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilchmann, N.
R;Seyler, Z. Physiol. Chem. 364, 71-80, 1983
A;Title: Die Primaerstruktur des kristallisierten Immunglobulins IgG1 KOL
A;Reference number: A91723; MUID: 8328931; PMID: 684994
A;Contents: myeloma protein kcl; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96, R, '98-197', 'D', '199-238', 'E', '268-271', 'D', '268-271', 'D', '273-330 < SCH
A;Note: this sequence has the Gim(3) and Gim(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 118-119, 1970
A;Title: The covalent structure of a human gamma-G-immunoglobulin. X. Intrachain disulfide
A;Reference number: A90565; MUID: 710640227; PMID: 4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglobulin
embromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID: 77070267; PMID: 1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:IGHGL
A;Cross-references: GDB:1200085; OMIM:147100
A;Map position: 14q32.3-14q22.33
A;Intnrs: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (κ^l)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1α
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: carbohydrate; Glycoprotein; heterotetramer; immunoglobulin
F;180/Binding site: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM3>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83, 144-204, 250-308/Disulfide bonds: #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 97.2%; Score 1225; DB 1; Length 330;
Best Local Similarity 97.0%; Pred. No. 3..5e-85; Indels 0; Gaps 0;
Matches 225; Conservative 3; N mismatches 4;

QY 1 EPKSCDKTHTCPCPAPELLGGPSVLFPPPKDTLMISRTPETCVVVDVSHEDPVKP
DB 99 EPKSCDKTHTCPCPAPELLGGPSVLFPPPKDTLMISRTPETCVVVDVSHEDPVKP 158

QY 61 NWYDGVEVHNWKTKEPREQNTSYRVSVTLHQNMNGKEYKCKVSNKALPAPIKT 120
DB 159 NWYDGVEVHNWKTKEPREQNTSYRVSVTLHQDLNGKEYKCKVSNKALPAPIKT 218

QY 121 ISKAKVQPREQVTLPSSRDELTKQSVLTLVKGFPSPDIAVEWENGQPNNTYKTP 180
DB 219 ISKAKVQPREQVTLPSSRDELTKQSVLTLVKGFPSPDIAVEWENGQPNNTYKTP 278

QY 181 PVLDGSFFFLYSLKLTVDKSRMQQNVFSCSVWHEALNNHYTOKSLSPGK 232
DB 279 PVLDGSFFFLYSLKLTVDKSRMQQNVFSCSVWHEALNNHYTOKSLSPGK 330

RESULT 2
S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Sequence: S69339; S72664
C;Accession: S69339; S72664
R;Khamlich, A.A.; Autourier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995

Y 181 PVLDGSFSPFLYSKLTVDKSRWQGNYFCSVMEALHNHYQRSLSLSPGK 232
 Y 204 PVLDGSFSPFLYSKLTVDKSRWQGNYFCSVMEALHNHYTQSLSLSPGK 255

RESULT 4

res207 Ig gamma chain C region - chimpanzee
 :Species: Pan troglodytes (chimpanzee)
 :Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
 :Accession: PT0207
 :Author: P.H.; Moustafa, Z.A.; Oestberg, L.
 :Title: Nucleotide sequence of chimpanzee FC and hinge regions.
 :Reference number: PT0207; PMID:91287716; PMID:2062315
 :Molecule type: tRNA
 :Residues: 1-234 <HHR>
 :Superfamily: immunoglobulin C region; immunoglobulin homology
 :Keywords: immunoglobulin
 :48:117/Domain: immunoglobulin homology <IMM>

Query Match 93.0% Score 1172; DB 2; Length 234;
 Best Local Similarity 95.6%; Pctd. No. 2.3e-81; Indels 0; Gaps 0;
 Matches 215; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

) 1 EPKSCDKTHTCPPAPELGGPSVELFPKKPDKTLMSIRPEVTCVVVDYSHEDPEVKF 60
) 10 EPKSCDTTHTCPPAAPELGGPSVFIFPKERDKTLMSIRPEVTCVVVDYSHEDPEVKF 69
) 61 NWYDGVEVHNVKTKPREEQYNSTYRVSVLTVLHQNTWNGKEYCKVSNKALPAIET 120
) 70 NWYDGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAIET 129

) 121 ISKAKVQPREPQTYLPPSRDELTKNQSLTCLVKGFPYPSDIAVEWESNGOPENNYKTTP 180
) 130 ISKAKGQPREPQTYLPPSRDELTKNQSLTCLVKGFPYPSDIAVEWESNGOPENNYKTTP 189

) 181 PVLDGSFSPFLYSKLTVDKSRWQGNYFCSVMEALHNHYQRS 225
) 190 PVLDGSFSPFLYSKLTVDKSRWQGNYFCSVMEALHNHTQKS 234

RESULT 5

13511 Ig gamma-3 chain C region (alleleotype G3m(b)) - human
 :Species: Homo sapiens (man)
 :Cross-references: GDB:IGH3
 :Accession: A23511
 :Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
 :Title: Sequence of a human immunoglobulin Gamma 3 heavy chain constant region gene: cDNA
 :Reference number: A23511; PMID:86148507; PMID:3081877
 :Molecule type: DNA
 :Residues: 1-377 <HUC>
 :Cross-references: GB:X03604; GB:MI2958; PIDN:CAA27268_1; PID:933070; PID:9577056
 :Genetics:
 :Cross-references: GDB:119339; OMIM:147120
 :Map position: 1q32.3-1q32.33
 :Proteins: Crawford, D.H.; LeFranc, M.P.; LeFranc, G.
 :Superfamily: immunoglobulin C region; immunoglobulin homology
 :Keywords: immunoglobulin
 :20-85/Domain: immunoglobulin homology <IMM>

Query Match 90.3% Score 1138; DB 2; Length 377;
 Best Local Similarity 89.7%; Pctd. No. 1.5e-78; Indels 0; Gaps 0;
 Matches 208; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

) 1 EPKSCDKTHTCPPCPAPELGGPSVLEPFPKPKDKTLMSIRPEVTCVVVDYSHEDPEVKF 60
) 146 EPKSCDTTPCPRCPPCPAPELGGPSVLEPFPKPKDKTLMSIRPEVTCVVVDYSHEDPEVKF 205

RESULT 6

A60764 Ig Gamma-3 chain C region, form LAT - human
 :Species: Homo sapiens (man)
 :Cross-references: GDB:IGH3
 :Accession: A60764
 :Ruck, S.; LeFranc, G.; LeFranc, M.P.
 :Immunogenetics 30, 250-257, 1989
 :Article: A human immunoglobulin IGH3 allele (Gmb3) with an IGH4 convertase
 :Reference number: A60764; MUID:9007613; PMID:2571587
 :A:Cross references: UNIPROT:OBN499
 :C:Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>
 :C:Keywords: immunoglobulin
 :F:20-85/Domain: immunoglobulin homology <HUC>
 :A:Statue: preliminary
 :A:Molecule type: DNA
 :A:Accession: 1-377 <HUC>
 :A:Cross references: UNIPROT:OBN499
 :C:Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>
 :C:Keywords: immunoglobulin
 :F:20-85/Domain: immunoglobulin homology <HUC>
 :Query Match 90.2% Score 1136; DB 2; Length 377;
 :Best Local Similarity 89.7%; Pctd. No. 2.1e-78; Indels 0; Gaps 0;
 :Matches 208; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCPAPELGGPSVLEPFPKPKDKTLMSIRPEVTCVVVDYSHEDPEVKF 60
 Qy 146 EPKSCDTTPCPRCPPCPAPELGGPSVLEPFPKPKDKTLMSIRPEVTCVVVDYSHEDPEVKF 205

Db 61 NWYDGVEVHNVKTKPREEQYNSTYRVSVLTVLHQNTWNGKEYCKVSNKALPAIET 120
 Db 206 KWYDGVEVHNARTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAIET 255

RESULT 7

G3HWWI Ig gamma-3 heavy chain disease proteins - human
 :Species: Homo sapiens (man)
 :Cross-references: GDB:IGH3
 :Accession: A23511
 :Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
 :Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy<-c>
 :Reference number: A90412; MUID:81021518; PMID:6774747
 :A:Contents: heavy chain disease protein Wis
 :A:Accession: A90412
 :A:Molecule type: protein
 :A:Residues: 1-289 <HFA>
 :A:Note: this molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain
 :A:Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 corresponds to the reference that follows
 :R.Michelsen, T.E.; Frangione, B.; Franklin, E.C.
 :J. Biol. Chem. 252, 883-889, 1977

A;Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication
 A;Reference number: A92219; MUID:77118561; PMID:40263
 A;Contents: normal Gamma-3 chains, sequence corresponding to residues 12-97 of protein W
 A;Molecule type: protein
 A;Residues: 12-97 <M1C>
 A;Note: The hinge region in gamma-3 chains is about four times as long as in other gamma
 iude segment (12-28)
 A;Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter-
 Biochem. Biophys. Res. Commun. 71, 907-914, 1976
 A;Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the
 A;Reference number: A90188; MUID:7702156; PMID:623915
 A;Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues
 A;Accession: A90198
 A;Molecule type: protein
 A;Residues: 59-125; 'EB', 128-226, 228-289 <W0L>
 A;Note: this protein lacks most of the V region, all of the CH1 region, and part of the
 R;Alexander, A.J.; Steinmerz, M.; Barrington, D.; Frangione, B.; Hood, L.;
 Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
 A;Title: Gamma heavy chain disease in man: cDNA sequence supports partial gene deletion
 A;Reference number: A93915; MUID:6808305
 A;Contents: heavy chain disease protein Omm
 A;Gene: A93915
 A;Molecule type: mRNA
 A;Residues: 12-70; 72-114; 116-125; 'E', 127-133; 'L', 135-136; 'E', 138; 'Y', 140-154; 'D', 156-157
 A;Note: a carboxyl-terminal lys is removed posttranslationaly
 A;Comment: this sequence may represent an allelic form or another gamma chain subclass
 C;Genetics:
 A;Cross-references: GDB:119339; OMIM:147120
 A;Map position: 14q3.2-14q3.3
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
 F;1/Modified site: Pyrrolidone carboxylic acid (Gln) #status experimental
 F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 89.1%; Score 1123; DB 1; Length 289;
 Best Local Similarity 88.3%; Pred. No. 1.5e-77;
 Matches 204; Conservative 14; Mismatches 13; Indels 0; Gaps 0;
 Qy 1 EPKSDIDTHHTCPCPAPELLPGPSVLFPPKPKDTLMSRTPEVTVWDVSHEDPVKF 60
 Db 59 PRPSCTDPPPCPRCPPAPELLPGPSVLFPPKPKDTLMSRTPEVTVWDVSHEDPVQF 118
 Qy 61 NYYVDGVBEVVKTKPREEQNSTYRVSVLTVLHQNMNGKEYKCVSNKALPAPBKT 120
 Db 119 KNYVGDGVQVHARTKREQENSTFVVSVLTVLHQNLGRETCKVSNAKALPAPBKT 178
 Qy 121 ISKAKTGPREPQVTLLPPSRDELTQVSLTCLYKGFFYPSDIAVEWNSQOPENNNTTP 180
 Db 179 ISKTKGPREPQVTLLPPSRDEMTQVSLTCLYKGFFYPSDIAVEWNSQOPENNNTTP 238
 Qy 181 PFLDSWSSEFLYSKLTDKSRSWQCNIFSCSVMHEALTHYQPSLSLSPG 231
 Db 239 PMLDSDSFSEFLYSKLTDKSRSRQCNIFSCSVMHEALTHNRFTOKSLSSPG 289

RESULT 8
 G2HU
 Ig gamma-2 chain C region - human
 C;Species: Homo sapiens (man)
 C;Text: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 09-Jul-2004
 C;Accession: A93906; A92809; A90752; A93132; A02148
 R;Ellison, J.; Hood, L.
 Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
 A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con-
 A;Reference number: A93906; MUID:82197621; PMID:6804348
 A;Accession: A93906
 A;Molecule type: DNA
 A;Residues: 1-326 <ELL>

A;Cross-references: UNIPROT: P01859; GB:100554; GB:J00330; MUID:932759; PMID:CA58438.1; 1
 A;Note: Lys-326 is probably removed posttranslationally
 R;Wang, A.C.; Tung, E.; Fludenberg, H.H.
 J. Immunol. 125, 1048-1054, 1980
 A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and 1
 A;Reference number: A92809; MUID:81007873; PMID:6774012
 A;Contents: myeloma protein T11
 A;Accession: A92809
 A;Molecule type: Protein
 A;Residues: 1-24; 'E', 26-57; 'EV', 60-85; 132-171; 'ZZZ', 175; 'B', 177-193; 'D', 195-196; 'Q', 198-
 A;Note: this sequence has since been revised
 R;Hofmann, T.; Parr, D.M.
 Mol. Immunol. 16, 923-925, 1979
 A;Title: The amino acid sequences of the three heavy chain constant region domains of a
 A;Reference number: A90752; MUID:80001357; PMID:113060
 A;Contents: myeloma protein Zie
 A;Accession: A90752
 A;Molecule type: Protein
 A;Residues: 1-24; 'E', 26-57; 'EV', 60-85; 132-171; 'ZZZ', 175; 'B', 177-193; 'D', 195-196; 'Q', 198-
 A;Note: this sequence has since been revised
 R;Hofmann, T.; Parr, D.M.
 submitted to the Atlas, March 1980
 A;Reference number: A93132
 A;Contents: annotation Zie, revisions to residues 25, 59, 60, and 264-268
 A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidated
 R;Milstein, C.; Frangione, B.
 Biochem. J. 121, 217-225, 1971
 A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
 A;Reference number: A90253; MUID:7203500; PMID:540472
 A;Contents: annotation: myeloma protein Sa, disulfide bonds
 R;Frangione, B.; Milstein, C.; Pink, J.R.L.
 Nature 221, 145-148, 1969
 A;Title: Structural studies of immunoglobulin G.
 A;Reference number: A93157; MUID:6906424; PMID:5782707
 A;Contents: annotation: Sa, disulfide bonds
 C;Genetics:
 A;Gene: GDB:IGHG2
 A;Cross-references: GDB:119338; OMIM:147110
 A;Map position: 14q32.3-14q32.33
 C;Complex: An immunoglobulin heterotrimer subunit consists of two identical light (κ) chains
 and one heavy chain. In some cases, such as IgM, the subunits associate into a single
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: duplication; glycoprotein; immunoglobulin homotramer; immunoglobulin
 F;20-85/Domain: immunoglobulin homology <IM1>
 F;133-202/Domain: immunoglobulin homology <IM2>
 F;239-306/Domain: immunoglobulin homology <IM3>
 F;14/Disulfide bonds: interchain (to light chain) #status experimental
 F;27-83, 140-200, 246-304/Disulfide bonds: #status experimental
 F;103, 103-106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental
 F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.9%; Score 1107; DB 1; Length 326;
 Best Local Similarity 88.4%; Pred. No. 2.8e-76;
 Matches 205; Conservative 12; Mismatches 11; Indels 4; Gaps 2;
 Qy 1 EPKSDIDTHHTCPCPAPELLPGPSVLFPPKPKDTLMSRTPEVTVWDVSHEDPVKF 60
 Db 99 ERKCCVE--CPCPAPP-VAGPSVELFPPKEDTLMSRTPEVTVWDVSHEDPVQF 154
 Qy 61 NWYDGVEVNVKTKPREEQNSTYRVSVLTVLHQNMNGKEYKCVSNKALPAPBKT 120
 Db 155 NWYDGVEVHNATKTPREQFISTPRVSVLTWHDWLNGKEYCKVSNAKALPAPBKT 120
 Qy 121 ISKAKTGPREPQVTLLPPSRDELTQVSLTCLYKGFFYPSDIAVEWNSQOPENNNTTP 180
 Db 155 NWYDGVEVHNATKTPREQFISTPRVSVLTWHDWLNGKEYCKVSNAKALPAPBKT 214
 121 ISKAKVQPREPOVYTLPPSRDELTQVSVLTLCKVGFYPSDIAVEWNSQOPENNNTTP 180

:ochemistry 10, 9-17, 1971
 Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Ami
 Reference number: A90359; MUID:71058486; PMID:5538616
 Accession: A90359
 Molecule type: Protein
 Residues: 69-131;312-329 <TUR>
 Tracey, D.E.; Cebra, J.J.
 :ochemistry 13, 4796-4803, 1974
 Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.
 Reference number: A90384; MUID:75036072; PMID:4429665
 Accession: A90384
 Molecule type: Protein
 Residues: 134-226 <TRA>
 Trischmann, T.M.; Cebra, J.J.
 :ochemistry 13, 4804-4811, 1974
 Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
 Reference number: A90385; MUID:75036073; PMID:4429667
 Accession: A90385
 Molecule type: Protein
 Residues: 227-311 <TRA>
 Oliveira, B.; Lamm, M.E.
 :ochemistry 10, 26-31, 1971
 Title: Interchain disulfide bridges of guinea pig gamma-2 immunoglobulin.
 Reference number: A90354; MUID:71058474; PMID:4922544
 Content: annotation; disulfide bonds
 Note: Cys-16 is involved in a heavy-light chain bond
 Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
 Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
 Complex: An immunoglobulin heterotrimer subunit consists of two identical light (lambda) in disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a superfamily: immunoglobulin C region; immunoglobulin homology <IM1>
 Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin
 21-81/Domain: immunoglobulin homology <IM1>
 135-240/Domain: immunoglobulin homology <IM2>
 241-310/Domain: immunoglobulin homology <IM3>
 28-79/Disulfide bonds: #status experimental
 142-222/Disulfide bonds: #status experimental
 178/Binding site: carbohydrate (Asn) (covalent) #status experimental
 248-308/Disulfide bonds: #status experimental

Query Match 68.1%; Score 858; DB 1; Length 329;

Best Local Similarity 67.4%; Prod. No. 1.7e-57; Mismatches 42; Indels 6; Gaps 2;

Matches 157; Conservative 28; Misinsertions 42; Indels 6; Gaps 2;
 1 EPKSDDKTHCPPPAPPELGGGSVLEPPKPKDTLMISRPEVTICVVVDVSHEDEPEVKF 60
 101 ZPBPC---TCPKCPPNLLGGGSVLEPPKPKDTLMISLPRVTCVVVDVSQDBPEVQF 156
 61 NWYDGVEYHNVKTKPREEQNSTRYVSVLTYLHQNMNGKEYKCKVSNKALPAPIKT 120
 157 TWFDNKPVGNAAEKTPKREQYNTFRVESVLPIQHQWLKGKEFKCKVSNKALPAPIKT 216
 121 ISKAKVQPREPQVTLPPSRLDELTKNQVSITCLVKGYPSPDSIAVENESNGQP-ENNYKT 178
 217 ISKTKGAPMPDVTLPPLPERDLSKSKVSVTCLINFPPADHVVEASNRPVSEKEYQN 276
 179 TPPVLDVGSSFLYPSKLTYDKSRMWWQQGVNFCSVMHRAHNHYQQRSLSLSPG 231
 277 TPPLEDADGSYFLYPSKLTVYDKSAWDQGTVYTCSVMHRAHNWTQKAISRSPG 329

RESULT 15

17158 3 gamma 1 chain constant region - Pig (fragment)

;Species: Sus scrofa domesticus (domestic pig)

;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

;Accession: I47158

;Kacskovics, I.; Sun, J.; Butler, J.E.

;Immunol. 153, 3565-3573, 1994

;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s

;Reference number: 147158; MUID:95015845; PMID:7930579

;Accession: I47158

;Status: Preliminary; translated from GB/EMBL/DDBJ

A: Molecule type: mRNA

A: Residues: 1-338 <KAC>

A: Cross references: EMBL:U03778; NID:g433121; PID:9433122

C: Genetics:

A: Gene: IgG1

C: Superfamily: immunoglobulin C region; immunoglobulin homology

F: 133-202/Domain: immunoglobulin homology <IM>

Query Match 67.3%; Score 847.5; DB 2; Length 328;

Best Local Similarity 69.3%; Prod. No. 1.1e-56;

Matches 156; Conservative 30; Mismatches 36; Indels 3; Gaps 2;

Qy 10 TOPPCPAPELIGGGSVLFPPKPKDTLMISRPEVTICVVVDVSHEDEPEVKFENNYVVDGVF 69

Db 105 TOPICPGE-VAGPSYFIFPPKPKDTLMISQPEVTICVVVDVSHEAEYQFSWVTDGVF 163

Qy 70 ENVKTKPREEQNSTYRVSVLTVLHQNMNGKEYKCKVSNKALPAPIKTISAKVOPR 129

Db 164 HFAETRKEEQDNSTRVSVLPIQFQDWIKRGREFCKYNNVDPAPIRTISAIAGSR 223

Qy 130 EPQVYTLPPSRSRDLTKNOVSITCLVKGYPSPSDIAVENESNGQ-ENNYKTTPPVLDVG 187

Db 224 EPQVYTLPPPAEELSRSSKVTLCLVTFYPDPDIHEWKENGQPEPENTYRTTPQQDVDG 283

Qy 188 SPPFLSLLTVKSRWQGNFSCSVMHEALTHNHYQRSLSLSPK 232

Db 284 TFLYSKLAVDVKARWDHGDXPECAVMEALTHNHYTQKS1SKTQGK 328

Search completed: October 27, 2004, 17:04:51.
 Job time : 21.728 secs

Job time : 21.728 secs

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protein - protein search, using sw model

on: October 27, 2004, 16:32:53 ; Search time 105.267 Seconds
(without alignments)
1268.081 Million cell updates/sec

file: US-10-000-439-3
effect score: 1260
quence: 1 EPKCDKTHTCPPCPAPELIL.....MHEALJNHYQRSLSLSPGK 232

oring table: BLASTM62
Gapop 10.0 , Gapext 0.5
arched: 1825181 seqs, 57537466 residues

real number of hits satisfying chosen parameters: 1825181

maximum DB seq length: 0
maximum DB seq length: 2000000000
er-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase : UniProt_02:
1: uniprot_sprot:
2: uniprot_trembl:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query	Match	Length	DB	ID	Description
1	1225	97.2	330	1	BCL_HUMAN		P01857; homologous to: Human gamma C chain fragment H4.
2	1225	97.2	447	2	BAC85237	AAH19337	Human gamma C chain fragment H4.
3	1225	97.2	464	2	BAC86226	AAH19337	Human gamma C chain fragment H4.
4	1225	97.2	465	2	Q6GMX6		Human gamma C chain fragment H4.
5	1225	97.2	466	2	Q6INT8		Human gamma C chain fragment H4.
6	1225	97.2	466	2	AAB64416		Human gamma C chain fragment H4.
7	1225	97.2	467	2	BAC85173		Human gamma C chain fragment H4.
8	1225	97.2	467	2	BAC85237		Human gamma C chain fragment H4.
9	1225	97.2	467	2	AAH31361		Human gamma C chain fragment H4.
10	1225	97.2	468	2	BAC85175		Human gamma C chain fragment H4.
11	1225	97.2	468	2	BAC85444		Human gamma C chain fragment H4.
12	1225	97.2	469	2	Q7Z7P5		Human gamma C chain fragment H4.
13	1225	97.2	470	2	Q6PJ44		Human gamma C chain fragment H4.
14	1225	97.2	470	2	Q7Z5W1		Human gamma C chain fragment H4.
15	1225	97.2	470	2	BAC85235		Human gamma C chain fragment H4.
16	1225	97.2	470	2	BAC85387		Human gamma C chain fragment H4.
17	1225	97.2	470	2	AAH63336		Human gamma C chain fragment H4.
18	1225	97.2	470	2	AAH14258		Human gamma C chain fragment H4.
19	1225	97.2	470	2	AAH18747		Human gamma C chain fragment H4.
20	1225	97.2	470	2	AAH25114		Human gamma C chain fragment H4.
21	1225	97.2	471	2	BAC85188		Human gamma C chain fragment H4.
22	1225	97.2	471	2	AAH22289		Human gamma C chain fragment H4.
23	1225	97.2	471	2	BAC05044		Human gamma C chain fragment H4.
24	1225	97.2	472	2	Q6N0B9		Human gamma C chain fragment H4.
25	1225	97.2	472	2	CPE45781		Human gamma C chain fragment H4.
26	1225	97.2	472	2	BAC85222		Human gamma C chain fragment H4.
27	1225	97.2	472	2	BAC86225		Human gamma C chain fragment H4.
28	1225	97.2	473	2	BAC05013		Human gamma C chain fragment H4.
29	1225	97.2	474	2	BAC85171		Human gamma C chain fragment H4.
30	1225	97.2	474	2	BAC85401		Human gamma C chain fragment H4.
31	1225	97.2	474	2	BAC05012		Human gamma C chain fragment H4.

ALIGNMENTS

32	1225	97.2	475	2	Q6GMW7		Human gamma C chain fragment H4.
33	1225	97.2	475	2	AAH22038		Human gamma C chain fragment H4.
34	1225	97.2	476	2	Q6GMX1		Human gamma C chain fragment H4.
35	1225	97.2	476	2	BAC05117		Human gamma C chain fragment H4.
36	1225	97.2	477	2	BAC85394		Human gamma C chain fragment H4.
37	1225	97.2	477	2	BAC85697		Human gamma C chain fragment H4.
38	1225	97.2	477	2	BAC05018		Human gamma C chain fragment H4.
39	1225	97.2	478	2	BAC85174		Human gamma C chain fragment H4.
40	1225	97.2	478	2	BAC85436		Human gamma C chain fragment H4.
41	1225	97.2	478	2	BAC86514		Human gamma C chain fragment H4.
42	1225	97.2	479	2	AAH06402		Human gamma C chain fragment H4.
43	1225	97.2	479	2	AAH14667		Human gamma C chain fragment H4.
44	1225	97.2	479	2	Q96Q8		Human gamma C chain fragment H4.
45	1224	97.1	474	2	BAC85350		Human gamma C chain fragment H4.

RESULT 1							
GC1_HUMAN		STANDARD;		PRT;		330 AA.	
ID	GCL_HUMAN						
AC	P01857;						
DT	21-JUL-1986	(Rel. 01, Created)					
DT	01-OCT-2004	(Rel. 45, Last sequence update)					
DB	Ig Gamma-1 chain C region.						
GN	Name=IGCHG1;						
OC	Homo sapiens (Human)						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;						
NCBI_TAXID	9606;						
RN							
[1]							
SEQUENCE FROM N.A.							
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).						
RP	MEDLINE=8224238; PubMed=6287432;						
RA	Ellison J.W.; Besson B.J.; Hood L.E., Gottlieb P.D.,						
RA	"The nucleic acid sequence of a human immunoglobulin C gamma 1 gene."						
RL	Nucleic Acids Res. 10:4071-4079(1982).						
RN							
[2]							
SEQUENCE OF 1-136-139 (EU).							
RP	MEDLINE=7104024; PubMed=489771;						
RA	Cunningham B.A.; Rutishauser U., Gall W.E., Gottlieb P.D.,						
RA	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanoogen bromide fragments H1-H4".						
RT	Edelman G.M.; Edelman G.M.;						
RT	"The covalent structure of a human gamma G-immunoglobulin. VIII. The chymotryptic peptides and RT acid sequence of heavy-chain cyanoogen bromide fragments H5-H7".						
RT	Biochemistry 9:3161-3170(1970)						
RN							
[3]							
SEQUENCE OF 136-139 (EU).							
RP	MEDLINE=7104025; PubMed=5530842;						
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,						
RA	"The primary structure of a monoclonal antibody to IgG1 immunoglobulin myeloma protein Niel. III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and RT discussion of the complete structure."						
RT	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).						
RN							
[4]							
SEQUENCE (MYELOMA PROTEIN NIE).							
RP	MEDLINE=77070269; PubMed=224675;						
RA	Ponstingl H., Hilschmann N.,						
RT	"The rule of antibody structure. The primary structure of a monoclonal antibody to IgG1 immunoglobulin myeloma protein Niel. III. The chymotryptic peptides and RT discussion of the complete structure."						
RT	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).						
RN							
[5]							
SEQUENCE (MYELOMA PROTEIN KOL) AND DISULFIDE BONDS.							
RP	MEDLINE=83285131; PubMed=684904;						
RA	Scmidt W.E., Jung H.-D., Palm W., Hilschmann N.,						
RA	"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";						
RT	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).						
RL							
[6]							
DISULFIDE BONDS.							
RP	MEDLINE=11061027; PubMed=4923144;						
RA							

RA Gall W.E., Edelman G.M.; "The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds"; *Biochemistry* 9:3188-3196(1970).
 RN [7]
 RN DISULFIDE BONDS.
 RX MEDLINE:77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.; "Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie), I: purification and characterization of the protein, the L- and H-chains, the cyanogen bromopeptidase products, and the disulfide bridges"; *J. Hoppe-Seyler's Z. Physiol. Chem.* 357:1515-1540(1976).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE:811208100; PubMed=7236658;
 RA Deisenhofer J.; "X-ray crystallographic refinement and atomic models of a human IgC fragment and its complex with fragment B of protein A from *Staphylococcus aureus* at 2.9- and 2.8-A resolution"; *Biochemistry* 20:2361-2370(1981).
 RL 1.- MISCELLANEOUS: Nie has the GIM(17) allotypic marker, 97-K, and the GIM(1) markers, 239-D and 241-L, KOL and EU sequences have the GIM(3) marker and the GIM (non-1) markers.
 CC -1.- MISCELLANEOUS: Nie also differs in the amidation states of 35, 116, 198, 269 and 272.
 CC -1.- MISCELLANEOUS: EU also differs in the amidation states of residues 155, 166, 177, 195, 198, 269, and 272 and in the order of residues 268-272.
 CC -1.- MISCELLANEOUS: KOL also differs in the amidation states of residues 198, 267 and 272.
 CC -----
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 CC -----
 DR EMBL; J00228; AAC82327; ALT_INIT.
 DR PIR; A93433; GHNU.
 DR PDB; 1A77; X-ray; H=1-103.
 DR PDB; 1D5B; X-ray; B=A=1-101.
 DR PDB; 1DSI; X-ray; H=1-101.
 DR PDB; 1D6V; X-ray; H=1-101.
 DR PDB; 1DN2; X-ray; A/B=126-326.
 DR PDB; 1E4K; X-ray; A/B=106-329.
 DR PDB; 1FC1; X-ray; A/B=106-329.
 DR PDB; 1FC2; X-ray; D=106-329.
 DR PDB; 1FCC; X-ray; A=121-326.
 DR PDB; 1HZH; X-ray; H/K=1-330.
 DR PDB; 1J7Z; X-ray; B/D=1-103.
 DR PDB; 1LIS; X-ray; A/B=107-330.
 DR PDB; 1LIX; X-ray; A/B=107-330.
 DR PDB; 1L6X; X-ray; A=120-326.
 DR PDB; 1OQX; X-ray; A/B=119-330.
 DR PDB; 2RCS; X-ray; H=1-103.
 DR Genew; HGNC:5525; IgHg1.
 DR MIM; 147100; -
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; :antigen binding; TAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR07110; Ig-like.
 DR InterPro; IPR033006; Ig_MHC.
 DR Pfam; PF00047; 19; 3.
 DR PROSITE; PS050835; Ig_LIKE; 3.
 DR PROSITE; PS00290; Ig_MHC; 2.
 KW Immunoglobulin C region; Immunoglobulin domain.
 FT NON_TER 1 1
 PT DOMAIN 1 98 CH1.
 PT DOMAIN 99 110 Hinge.
 SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FF33D CRC64;
 Query Match 97.2%; Score 1225; DB 1; Length 330;
 Best Local Similarity 97.0%; Pred. No. 1.8e-89;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EPKSDKTHTCPCPAPBLLGGPSVLFPPPKPDLMISRTPEVTVVVDVSHEDPEVK 60
 DB 99 EPKSDKTHTCPCPAPBLLGGPSVLFPPPKPDLMISRTPEVTVVVDVSHEDPEVK 158

		RN	[1]
		RP	SEQUENCE FROM N.A.
		RC	TISSUE=Syncytial membrane tissue;
		RA	Tashiro H., Yanazaki M., Watanabe K., Kumagai A., Itakura S.,
		RA	Fujimori Y., Nishikawa T., Komiya M., Sugiyama T., Irie R.,
		RA	Okutsu T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
		RA	Kawai Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
		RA	Matsuoka Y., Nakamura Y., Sekine M., Kuroki H., Kanda K., Wagasuma M.,
		RA	Murakawa K., Kaneko K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
		RA	Iwakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
		RA	Tsogai T.;
		RT	NBDO human cDNA sequencing project.";
		DR	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
		DR	EMBL; AKI12633; BAC6226; 1; -;
		SQ	P2884C17E89EEF CRC64;
		SEQUENCE	447 AA; 49289 MW;
	RESULTS 2		
) C85237	PRELIMINARY;	Score 1225; DB 2; Length 447;
) BA85237	PRT;	97.2%; Score 1225; DB 2; Length 447;
		Best Local Similarity	97.0%; Pred. No. 2.5e-89;
		Matches	3; Mismatches 4; Indels 0; Gaps 0;
		Query Match	97.2%; Score 1225; DB 2; Length 447;
		Best Local Similarity	97.0%; Pred. No. 2.5e-89;
		Matches	225; Conservative
		Query	1 EPKSCDKTHTCPPCAPELGGPSVLEPPPKPDTLMISRTPEVTVYDVSHEDPEYKF 60
		Db	216 EPKSCDKTHTCPPCAPELGGPSVLEPPPKPDTLMISRTPEVTVYDVSHEDPEYKF 275
		Query	61 NWYVDGTEVANKTKPDEEQNSTRVSVLTUQNWNNGKEYKCRVSNKALAPIEK 120
		Db	276 NWYVDGTEVANKTKPDEEQNSTRVSVLTUQNWNNGKEYKCRVSNKALAPIEK 335
		Query	121 ISKAKYOPREPVQYTLPPSDDLTRKNQVSITCLVKGFYPSDIAVEWSNGQPENNYKTP 180
		Db	336 ISKAKGDPREPVTIPLPSRBLTRQNQVSITCLVKGFYPSDIAVEWSNGQPENNYKTP 395
		Query	181 PVLDGSFFFLYSKLTVDKSRWQQNVFSCSVMHEALTHNHYQRSLSSPGK 232
		Db	396 PVLDGSFFFLYSKLTVDKSRWQQNVFSCSVMHEALTHNHYQRSLSSPGK 447
		RESULT 4	
		AAH19337	PRELIMINARY;
		ID	AAH19337
		AC	AAH19337;
		DT	02-MAR-2004 (TREMBrel. 27, Created)
		DT	02-MAR-2004 (TREMBrel. 27, Last sequence update)
		DE	Hypothetical protein.
		DT	02-MAR-2004 (TREMBrel. 27, Last annotation update)
		OS	Homo sapiens (Human)
		OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
		NCBI TaxID	9006;
		NCBI TaxID	9006;
		RN	SEQUENCE FROM N.A.
		RC	SEQUENCE=Dermoid tumor;
		RA	Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami K., Nagai K., Isogai T., Sugano S.;
		RA	"NBDO human cDNA sequencing project"; Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases. EMBL; AKI12980; BAC85237; 1; -;
		RA	SEQUENCE 407 AA; 44159 MW; DB884D367B456FCB CRC64;
	RESULTS 2		
) C85237	PRELIMINARY;	Score 1225; DB 2; Length 407;
) BA85237	PRT;	97.2%; Score 1225; DB 2; Length 407;
		Best Local Similarity	97.0%; Pred. No. 2.3e-89;
		Matches	225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
		Query Match	97.2%; Score 1225; DB 2; Length 407;
		Best Local Similarity	97.0%; Pred. No. 2.3e-89;
		Matches	225; Conservative
		Query	1 EPKSCDKTHTCPPCAPELGGPSVLEPPPKPDTLMISRTPEVTVYDVSHEDPEYKF 60
		Db	176 EPKSCDKTHTCPPCAPELGGPSVLEPPPKPDTLMISRTPEVTVYDVSHEDPEYKF 235
		Query	61 NWYVDGVEVANKTKPDEEQNSTRVSVLTUQNWNNGKEYKCRVSNKALAPIEK 120
		Db	236 NWYVDGEVANKTKPDEEQNSTRVSVLTUQNWNNGKEYKCRVSNKALAPIEK 295
		Query	121 ISKAKYOPREPVQYTLPPSDDLTRKNQVSITCLVKGFYPSDIAVEWSNGQPENNYKTP 180
		Db	296 ISKAKCOPREFQYTLPPSDDLTRKNQVSITCLVKGFYPSDIAVEWSNGQPENNYKTP 355
		Query	181 PVLDGSFFFLYSKLTVDKSRWQQNVFSCSVMHEALTHNHYQRSLSSPGK 232
		Db	356 PVLDGSFFFLYSKLTVDKSRWQQNVFSCSVMHEALTHNHYQRSLSSPGK 407
		RESULT 3	
		AC86226	PRELIMINARY;
	D	PRT;	447 AA.
	C	Best Local Similarity	97.2%; Score 1225; DB 2; Length 447;
	T	Matches	225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
	T	Query Match	97.2%; Score 1225; DB 2; Length 447;
	T	Best Local Similarity	97.0%; Pred. No. 2.3e-89;
	T	Matches	225; Conservative
	T	Query	02-MAR-2004 (TREMBrel. 27, Created)
	T	Db	02-MAR-2004 (TREMBrel. 27, Last sequence update)
	T	Query	02-MAR-2004 (TREMBrel. 27, Last annotation update)
	T	Db	02-MAR-2004 (TREMBrel. 27, Last annotation update)
		DE	Chain C region.
		OS	Homino sapiens (Human)
		OC	Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
		NCBI TaxID	9006;
		RN	SEQUENCE FROM N.A.
		RC	SEQUENCE=Primary B-cells;
		RA	MEDLINE=22388257; PubMed=124777932;
		RA	Strasburg R.L., Feinsold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shevchenko C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Brownstein M.J., Usdin T.B., Tsohivski S., Carrinci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullay S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muany D.M., Soddergren E.J., Lu X., Gibbs R.A., Fahay J., Heijton B., Kettenman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimes J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Snailus D.E., Schnerr A., Schein J.E., Jones S.J., Marra M.A., Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences.";
		RA	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[2]	RN SEQUENCE FROM N.A.	DR InterPro; IPR007110; Ig-like.
RP TISSUE=Primary B-Cells;	DR InterPro; IPR003597; Ig C1.	
RC Strausberg R.;	DR InterPro; IPR00006; Ig MHC.	
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.	DR InterPro; IPR003596; Ig v.	
RL EMBL; BC01937; AAH13337.1; -.	DR Pfam; PF07654; Ig1; 3.	
KW Hypothetical protein.	DR Pfam; PF00047; Ig; 4.	
SQ 464 AA; 50891 MW; 2F80673E742A85 CRC64;	DR SMART; SM00409; IgC1; 2.	
Query Match 97.2%; Score 1225; DB 2; Length 464;	DR SMART; SM00406; IgV; 1.	
Best Local Similarity 97.0%; Pred. No. 2.7e-89;	DR PROSITE; PS00845; Ig_LIKE; 4.	
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;	DR PROSITE; PS00230; Ig_MHC; UNKNOWN_2.	
Sequence 465 AA; S1083 MW; B3A9B7D0FDB1386B CRC64;	KW Hypothetical protein.	
Qy 1 EPKSCDKTHTCPCPABILLGGPSVLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKP 60	Query Match 97.2%; Score 1225; DB 2; Length 465;	
Db 233 EPKSCDKTHTCPCPABILLGGPSVLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKP 292	Best Local Similarity 97.0%; Pred. No. 2.7e-89;	
Qy 61 NWYDGVEVHNVKTPREEQNISTYRIVSUTLVHQMNCKEYCKVSKNALPAPIKT 120	Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;	
Db 293 NWYDGVEVHNVKTPREEQNISTYRIVSUTLVHQMNCKEYCKVSKNALPAPIKT 352	Sequence 465 AA; S1083 MW; B3A9B7D0FDB1386B CRC64;	
Qy 121 ISKAKVQPREPOVYTLPPSRDELTKIQVSUTCLYRGFYPDSIAVEWSNGQPNNYKTP 180	Qy 1 EPKSCDKTHTCPCPABILLGGPSVLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKP 60	
Db 353 ISYAKGQPREPOVYTLPPSRDELTRQVSUTCLYRGFYPDSIAVEWSNGQPNNYKTP 412	Db 234 EPKSCDKTHTCPCPABILLGGPSVLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKP 293	
Qy 181 PVLDVGSSFFLYSKLTVTDKSPWQQGNVFCSCVMHEALHNHYQQRSLISLSPGK 232	Qy 61 NWYDGVEVHNVKTPREEQNISTYRIVSUTLVHQMNCKEYCKVSKNALPAPIKT 120	
Db 413 PVLDGDGSFFLYSKLTVTDKSPWQQGNVFCSCVMHEALHNHYTQSLISLSPGK 464	Db 294 NWYDGVEVHNVKTPREEQNISTYRIVSUTLVHQMNCKEYCKVSKNALPAPIKT 353	
RESULT 5	Qy 121 ISKAKVQPREPOVYTLPPSRDELTKIQVSUTCLYRGFYPDSIAVEWSNGQPNNYKTP 180	
O6GMX6 ID O6GMX6 PRELIMINARY; PRT; 465 AA.	Db 354 ISYAKGQPREPOVYTLPPSRDELTRQVSUTCLYRGFYPDSIAVEWSNGQPNNYKTP 412	
AC Q6GMX6; DT 01-JUL-2004 (TREMBLref). 27, Last sequence update)	Qy 181 PVLDVGSSFFLYSKLTVTDKSPWQQGNVFCSCVMHEALHNHYQQRSLISLSPGK 232	
DT 05-JUL-2004 (TREMBLref). 27, Last annotation update)	Db 414 PVLDGDGSFFLYSKLTVTDKSPWQQGNVFCSCVMHEALHNHYTQSLISLSPGK 464	
DT 05-JUL-2004 (TREMBLref). 27, Last annotation update)	RESULT 6	
DE Hypothetical protein.	Q6IN78 PRELIMINARY; PRT; 466 AA.	
OS Homo sapiens (Human).	AC Q6IN78; DT 05-JUL-2004 (TREMBLref). 27, Created)	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	CC NCBI TaxID=9006; DT 05-JUL-2004 (TREMBLref). 27, Last annotation update)	
OX NCBI_Taxid:9606;	DE IGRLI protein.	
RN [1]	GN Name=IGRLI;	
RP SEQUENCE FROM N.A.	OS Homo sapiens (Human)	
RC TISSUE=Primary B-Cells;	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
RX MEDLINE=22388257; PubMed=12477932;	RC TISSUE=Peripheral Nervous System;	
RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,	RX MEDLINE=22388257; PubMed=12477932;	
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	RA Altchul S.F., Zeeberg B., Buetow K.H., Wagner L., Shemesh C.M., Schuler G.D.,	
RA Diatchenko L., Marusina K., Farmer A.A., Casavant T.L., Scheetz T.E.,	RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G., Bhat N.K.,	
RA Stapleton M., Soares M.B., Ronald M.F., Casavant T.L., Scheetz T.E.,	RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA Brownstein M.J., Usdin T.B., Toshimatsu S., Carninci P., Prange C.,	RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,	RA Stapleton M., Sores M.B., Ronald M.F., Casavant T.L., Scheetz T.E.,	
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	RA Brownstein M.J., Usdin T.B., Toshimatsu S., Carninci P., Prange C.,	
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Gunaratne P.H.,	RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,	
RA Villarino D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,	RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Gunaratne P.H.,	
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	RA Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA Rodriguez A.C., Grinowski M.I., Skalska U., Smailius D.E., Schein J.E.,	RA Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,	
RA Jones S.J., Maura M.A.; "Generation and initial analysis of more than 15,000 full-length human	RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RT and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RL RN [2]	RA Rodriguez A.C., Grinowski J., Schmitz J.R.M., Myers R.M., Butterfield Y.S.,	
RP SEQUENCE FROM N.A.	RA Krywinski M.I., Skalska U., Smailius D.E., Schein J.E.,	
RC TISSUE=Primary B-Cells;	RA Jones S.J., Maura M.A.;	
RA Strausberg R.;	RA "Generation and initial analysis of more than 15,000 full-length human	
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.	RT and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	
RL EMBL; BC073766; AAH13766.1; -.	RL	
DR InterPro; IPR003599; Ig; 4.	RN [2]	

RT	"Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences"; RN [2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Peripheral Nervous System;
RA	Strasbourg R.; Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL	EMBL: BC072419; AAH72119.1; -.
RR	InterPro; IPRO003589; Ig_1-like.
RA	InterPro; IPRO07110; Ig_1-like.
RL	InterPro; IPRO03597; Ig_c1.
RA	InterPro; IPRO03036; Ig_MHC.
RL	InterPro; IPRO03586; Ig_v.
RA	Pfam: PF00047; C1-set; 3.
RL	Pfam: PF00047; Ig_4.
RA	SMART; SM00400; Ig_2.
RL	SMART; SM00407; Igcl; 3.
RA	SMART; SM00446; Igv; 1.
RL	PROSITE; PS55835; Ig_LIKE; 4.
RA	PROSITE; PS00390; Ig_MHC; UNKNOWN 2.
RL	SEQUENCE 466 AA; 5053 MW; 53EB0CDE81076E CRC64;
RA	Query Match 97.2%; Score 1225; DB 2; Length 466; Best Local Similarity 97.0%; Prod. No. 2.7e-89; Indels 0; Gaps 0;
RA	Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
RA	1 EPKSCDKHTCPCPAPAPLLGGPSVFLPPPKPDTLMISRTPEVTCVVVDYSDHEDEVKF 60 235 EPKSCDKHTCPCPAPAPLLGGPSVFLPPPKPDTLMISRTPEVTCVVVDYSDHEDEVKF 294
RA	61 NWYTDGVVEHNVKTKPREEQNNTYRVSVLTVHQNMNGKEYKCKVSNKALPAPIKT 120 295 NWYTDGVVEHNAKTKPREEQNNTYRVSVLTVHQDLNGKEYKCKVSNKALPAPIKT 354
RA	121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWSNGOPENNYKTTP 180 355 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWSNGOPENNYKTTP 414
RA	181 PVLDGSFFSFLYSLKLTVDKRSRQGNVFSCTMHEALHNHQCRSLSLSPKG 232 415 PVLDGSFFSFLYSLKLTVDKRSRQGNVFSCTMHEALHNHQCRSLSLSPKG 466
RA	RESULT 8 BAC81173 PRELIMINARY; ID BAC81173 PRT; 467 AA. AC BAC81173; DT 02-MAR-2004 (TREMBrel. 27, Created) DT 02-MAR-2004 (TREMBrel. 27, Last sequence update) DT 02-MAR-2004 (TREMBrel. 27, Last annotation update)
RA	DE CDNA FLJ26001 fis, clone DM07585, highly similar to Ig gamma-1 chain DE C region.
RA	DE Homo sapiens (Human).
RA	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
RA	NCBI_TaxID:9806; [1]
RA	RN "NEEDO human cDNA sequencing project";
RA	RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases. DR EMBL: AK129512; BAC85173.1; -.
RA	DR SEQUENCE 467 AA; 50782 MW; 632AEAD6CD248F5 CRC64;
RA	Query Match 97.2%; Score 1225; DB 2; Length 467; Best Local Similarity 97.0%; Prod. No. 2.7e-89; Indels 0; Gaps 0;
RA	Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
RA	SEQUENCE FROM N.A.
RA	TISSUE=Peritoneal tumor;
RA	Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y., Hata H., Nakagawa M., Morinaga M., Kawamura M., Sugiyama T., Irie R., Onuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B., Nagai K., Isogai T., Sugano S.;
RA	RT "NEEDO human cDNA sequencing project";
RA	RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases. DR EMBL: AK129512; BAC85173.1; -.
RA	Query Match 97.2%; Score 1225; DB 2; Length 467; Best Local Similarity 97.0%; Prod. No. 2.7e-89; Indels 0; Gaps 0;
RA	Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
RA	SEQUENCE FROM N.A.
RA	TISSUE=Spleen;
RA	MEDLINE=2388257; PubMed=12477932;
RA	Klaussberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Ait-Bachir S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K., Richards S., Worley P.J., Moore T., Wang Max S.I., Wang J., Hsieh P., Diarchenko L., Martinsa K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Sonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Villalona D.K., Muzny D.M., Sodergren E.J., Garcia A.M., Gay L.J., Gibbs R.A., Paehey J., Heilton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzewinski M.I., Skalska U., Schein J.E., Schnieke A., Jones S.J., Matra M.A.,

RESULT 9	AAH37361	PRELIMINARY;	PRT;	468 AA.
QY	181 PVLDSVGSFLYLSSKLTVDKSRWQQNVFSCSVMEALHNHYQDRLSLSPGK 232			
Db	416 PVLDSVGSFLYLSSKLTVDKSRWQQNVFSCSVMEALHNHYQDRLSLSPGK 467			
ID	AAH37361	PRELIMINARY;	PRT;	467 AA.
AC				
DT	02-MAR-2004 (TREMBrel. 27, Created)			
DR	02-MAR-2004 (TREMBrel. 27, Last sequence update)			
DE	Homo sapiens (Human)			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.			
NCBI_TaxID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Spine;			
RX	MEDLINE=2388557; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Crouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Wagner L., Shenmen C.M., Shulman C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diarchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinco P., Prange C., Raha S.S., Loquejillo N.A., Peters G.J., Abramson R.D., Mulilahy S.J., Bosak S.A., McLearn P.J., McKernan K.J., Malick J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalona D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fafeby J., Hellon E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez E.C., Grimes D.J., Schildkraut J.J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalius D.E., Schnierch A., Schein J.B., Jones S.J., Marra M.A.			
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."			
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	Strausberg R.			
RL	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC037361; AAH37361.1; -			
DE	Hypothetical protein.			
CC	C region.			
NCBI_TaxID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Dermoid tumor;			
RA	Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y., Ota H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Kawakami B., Nagai K., Isogai T., Sato H., Nishikawa T., Sugiyama A., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Spine;			
RA	Strausberg R.L., Feingold E.A., Crouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Wagner L., Shenmen C.M., Shulman C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diarchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinco P., Prange C., Raha S.S., Loquejillo N.A., Peters G.J., Abramson R.D., Mulilahy S.J., Bosak S.A., McLearn P.J., McKernan K.J., Malick J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalona D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fafeby J., Hellon E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez E.C., Grimes D.J., Schildkraut J.J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalius D.E., Schnierch A., Schein J.B., Jones S.J., Marra M.A.			
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."			
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	Strausberg R.			
RL	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC037361; AAH37361.1; -			
DE	Hypothetical protein.			
CC	C region.			
NCBI_TaxID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., RA			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK1-9517; BAC8544.1; -			
SQ	SEQUENCE 468 AA; 51266 MW;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Kawakami B., Nak			

	Matches	Conservative	3;	Mismatches	4;	Indels	0;	Gaps	0;
Y	1	EPKSCDKTHTCPPCPAPPELIGGSVLFPPKPKDTLMISRPEVTCVVVDPSHEDPEVKP	60						
Y	237	EPKSCDKTHTCPPCPAPPELIGGSVLFPPKPKDTLMISRPEVTCVVVDPSHEDPEVKP	296						
Y	61	NWYDGVVEHANKTKPREQNSTYRVSUTLVHQWNNNGKEYKVNKAALPPIEKT	120						
Y	297	NWYDGVVEHANKTKPREQNSTYRVSUTLVHQWNNNGKEYKVNKAALPPIEKT	356						
Y	121	ISAKVQPEPQVTLPPSRDELTKNQSLTCLVKVQYPSDIAVEENGOPENNYKTP	180						
Y	357	ISAKKQPEPQVTLPPSRDELTKNQSLTCLVKVQYPSDIAVEENGOPENNYKTP	416						
/	181	PVLDSVGSSFFLYSKLTVDKSRSRQGNTYFSCSYMHAEAHNYCORSLSLSPK	232						
/	417	PVLDSDGSSFFLYSKLTVDKSRSRQGNTYFSCSYMHAEAHNYTQKSLSLSPK	468						
RESULT 12									
Q7ZTP5	Q7ZTP5	PRELIMINARY;	PRT;	469 AA.					
[1]	Q7ZTP5;	PRELIMINARY;	PRT;	469 AA.					
[2]	01-OCT-2003 (TREMBLrel. 25, Created)								
[3]	01-MAR-2004 (TREMBLrel. 26, Last sequence update)								
[4]	TIGIHL protein.								
[5]	Homo sapiens (Human).								
[6]	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxID=9606;								
[7]	SEQUENCE FROM N.A.								
[8]	TISSUE=Spleen;								
[9]	MEDLINE=22388257; PubMed=12477932;								
A	Strausberg R.L., Feingold E.A., Grouse L.H., Shemesh C.M., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Bhat N.K., Derge J.G., Schaefer C.F., Bhat N.K., Altenschul S.F., Zeeberg B., Buetow K.H., Shemesh C.M., Schuler G.D., Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Aalschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA								
A	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA								
A	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schatz T.E., RA								
A	Brownstein M.J., Usdin T.B., Toshimori S., Casavant T.L., Schatz T.E., RA								
A	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., RA								
A	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA								
A	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA								
A	Villalon D.K., Many D.M., Sodergren E.J., Lu X., Gibbs R.A., RA								
A	Whiting M., Heitton B., Ketteman M., Madan A., Rodriguez S., Sanchez A., RA								
A	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA								
A	Rodriguez A.C., Grimwood J., Schmitz J.J., Myers R.M., Butterfield Y.S., RA								
A	Krzewinski M.I., Skalska U., Smailus D.E., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). RT								
L	SEQUENCE FROM N.A.								
P	TISSUE=Spleen;								
P	Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.								
R	EMBL: BCC01328; AA51328; 1. - .								
R	InterPro: IPR003110; Ig-like.								
R	InterPro: IPR003597; Ig-cl.								
R	InterPro: IPR003006; Ig_MHC.								
R	InterPro: IPR003596; Ig_v.								
R	Pfam: PF07654; Cl-set; 3.								
R	SMART: SM00406; Ig_v.								
R	PROSITE: PS5035; Ig_LIKE; 4.								
R	PROSITE: PS00390; Ig_MHC; UNKOWN 2.								
R	SEQUENCE 459 AA;	CBD5BEB12BAAF795C CRC64;							
Query Match	97.2%	Score 1225;	DB 2;	Length 469;					
Best Local Similarity	97.0%	Pred NC 2	7e-89;						

KW	Hypothetical protein.	DR	PROSITE; PS50835; IG_LIKE; 4.
SQ	SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;	DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.
	Query Match Score 1225; DB 2; Length 470;	KW	Hypothetical protein.
	Best Local Similarity 97.0%; Pred. No. 2.7e-89; 3; Mismatches 225; Conservative Matches 225;	SEQUENCE	470 AA; 51204 MW; 778CP34521483E1A CRC64;
Qy	1 EPKSCDKTHTCPPCPAPELGGPSVLEPPKPKDTLMISRTPEVTCVVVDYSHEDPEVKF 60	Qy	Query Match Score 1225; DB 2; Length 470;
Db	239 EPKSCDKTHTCPPCPAPELGGPSVLEPPKPKDTLMISRTPEVTCVVVDYSHEDPEVKF 298	Db	Best Local Similarity 97.0%; Pred. No. 2.7e-89; 3; Mismatches 225; Conservative Matches 225;
Qy	61 NWYVGVEVHNVKTKPREEQNSTYRVSVLTILHQNQNNNGKEYCKVSNKALPPIKT 120	Qy	1 EPKSCDKTHTCPPCPAPELGGPSVLEPPKPKDTLMISRTPEVTCVVVDYSHEDPEVKF 60
Db	299 NWYVGVEVHNVKTKPREEQNSTYRVSVLTILHQDNLNGKEYCKVSNKALPPIKT 358	Db	239 EPKSCDKTHTCPPCPAPELGGPSVLEPPKPKDTLMISRTPEVTCVVVDYSHEDPEVKF 298
Qy	121 ISKAKVQPREPOVYTIPPSRDELTKNQVSLLTCLVKFQYSDIAVEWSNGOPENNYKTP 180	Qy	61 NWYVGVEVHNVKTKPREEQNSTYRVSVLTILHQNQNGKEYCKVSNKALPPIKT 120
Db	359 ISKAKGQPREPOVYTIPPSRDELTKNQVSLLTCLVKFQYSDIAVEWSNGOPENNYKTP 418	Db	299 NWYVGVEVHNAKTQPREEQNSTYRVSVLTILHQDNLNGKEYCKVSNKALPPIKT 358
Qy	181 PVLDVGSSFFLYSKLTVDKSRWQQGNVFSCSVMEALHYOQRSLSLSPGK 232	Qy	121 ISKAKVQPREPOVYTIPPSRDELTKNQVSLLTCLVKFQYSDIAVEWSNGOPENNYKTP 180
Db	419 PVLDGDSFFLYSKLTVDKSRWQQGNVFSCSVMEALHYTQKSLSLSPGK 470	Db	359 ISKAKGQPREPOVYTIPPSRDELTKNQVSLLTCLVKFQYSDIAVEWSNGOPENNYKTP 418
RESULT 14			
Q7Z5W1	PRELIMINARY; PRT; 470 AA.	Q7Z5W1	PRELIMINARY; PRT; 470 AA.
ID	BAC8235	ID	BAC8235
AC	BAC8235;	AC	BAC8235;
DT	01-OCT-2003 (TREMBLrel. 25, Created)	DT	02-MAR-2004 (TREMBLrel. 27, Created)
DT	01-MAR-2004 (TREMBLrel. 25, Last sequence update)	DT	02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DE	Hypothetical protein.	DE	02-MAR-2004 (TREMBLrel. 25, Last annotation update)
OS	Homo sapiens (Human)	OS	CDNA FLJ06276 (is, clone DMC06522, highly similar to Ig gamma-1 chain C region)
OC	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	DE	DE
OX		OS	Homo sapiens (Human).
RN	[1] NCBI_TaxID=9606;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RP	SEQUENCE FROM N.A.	OC	Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
RC	TISSUE=Spleen;	RN	[1] NCBI_TaxID=9606;
RC	MEDLINEB=22388257; PubMed=12477932;	RP	SEQUENCE FROM N.A.
RA	Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Schuler G.D.,	RC	TISSUE=Partoid tumor;
RA	Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Blatt N.K.,	RA	RA T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
RA	Aitischall S.F., Zeeberg B., Butow K.H., Maxine T., Hsieh F.,	RA	RA Otai T., Nakagawa K., Mizunaga M., Kawamura M.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Irie R., Otsuki T., Sato H., Niishikawa T., Sugiyama A.,	RA	RA Sugiyama T., Irie R., Otsuki T., Sato H., Niishikawa T., Sugiyama A.,
RA	Dianchenko L., Mausins K., Farmer A.A., Rubin G.M., Hong L., Kawakami B., Ngai K., Isogai T., Sugano S.;	RA	RA Kawakami B., Ngai K., Isogai T., Sugano S.;
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RT	RA	"NEDO human cDNA sequencing project";
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carminci P., Prange C., BL	BL	RT Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carminci P., Prange C., DR	DR	EMBL; AK129787; BAC8225.1.
RA	Bosak S.A., Logue L.N.A., Peters G.J., Abramson R.D., Mullany S.J., DR	DR	DR EMBL; AK129787; BAC8225.1.
RA	McEwan P.J.J., McKernan R.J., Malek J.A., Gunaratne P.H., Mullany S.J., SQ	SQ	SQ Sequence 470 AA; 51090 MW; 460F471D4528A16 CRC64;
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W.,	Qy	Query Match Score 1225; DB 2; Length 470;
RA	Villarreal D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	Db	Best Local Similarity 97.0%; Pred. No. 2.7e-89; 3; Mismatches 4; Indels 0; Gaps 0;
RA	Fahay J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,	Qy	1 EPKSCDKTHTCPPCPAPELGGPSVLEPPKPKDTLMISRTPEVTCVVVDYSHEDPEVKF 60
RA	Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,	Db	239 EPKSCDKTHTCPPCPAPELGGPSVLEPPKPKDTLMISRTPEVTCVVVDYSHEDPEVKF 298
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	Qy	61 NWYVGVEVHNVKTKPREEQNSTYRVSVLTILHQNQNGKEYCKVSNKALPPIKT 120
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	Db	299 NWYVGVEVHNAKTQPREEQNSTYRVSVLTILHQDNLNGKEYCKVSNKALPPIKT 358
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,	Qy	121 ISKAKVQPREPOVYTIPPSRDELTKNQVSLLTCLVKFQYSDIAVEWSNGOPENNYKTP 180
RA	Jones S.J., Marrs M.A.;	Db	359 ISKAKGQPREPOVYTIPPSRDELTKNQVSLLTCLVKFQYSDIAVEWSNGOPENNYKTP 418
RT	"Generation and initial analysis of more than 15,000 full-length human	Qy	181 PVLDVGSSFFLYSKLTVDKSRWQQGNVFSCSVMEALHYOQRSLSLSPGK 232
RL	and mouse cDNA sequences";	Db	419 PVLDGDSFFLYSKLTVDKSRWQQGNVFSCSVMEALHYTQKSLSLSPGK 470
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	RN	SNART; SM00406; IgV; 1.
RESULT 15			
Q7Z5W1	PRELIMINARY; PRT; 470 AA.	Q7Z5W1	PRELIMINARY; PRT; 470 AA.
ID	BAC8235	ID	BAC8235
AC	BAC8235;	AC	BAC8235;
DT	02-MAR-2004 (TREMBLrel. 27, Created)	DT	02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT	02-MAR-2004 (TREMBLrel. 25, Last annotation update)	DT	02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DE		DE	CDNA FLJ06276 (is, clone DMC06522, highly similar to Ig gamma-1 chain C region)
OS		DE	OS
OC		OS	Hominoidea; Hominidae; Homo.
OC		OC	Primate; Catarrhini; Hominidae; Homo.
OX		OC	Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
RN		OX	
RP	SEQUENCE FROM N.A.	RN	
RC	TISSUE=Spleen;	RP	SEQUENCE FROM N.A.
RC	MEDLINEB=22388257; PubMed=12477932;	RC	TISSUE=Partoid tumor;
RA	Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Schuler G.D.,	RA	RA T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
RA	Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Blatt N.K.,	RA	RA Otai T., Nakagawa K., Mizunaga M., Kawamura M.,
RA	Aitischall S.F., Zeeberg B., Butow K.H., Maxine T., Hsieh F.,	RA	RA Sugiyama T., Irie R., Otsuki T., Sato H., Niishikawa T., Sugiyama A.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Irie R., Otsuki T., Sato H., Niishikawa T., Sugiyama A.,	RA	RA Sugiyama T., Irie R., Otsuki T., Sato H., Niishikawa T., Sugiyama A.,
RA	Dianchenko L., Mausins K., Farmer A.A., Rubin G.M., Hong L., Kawakami B., Ngai K., Isogai T., Sugano S.;	RA	RA Kawakami B., Ngai K., Isogai T., Sugano S.;
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RT	RT	"NEDO human cDNA sequencing project";
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carminci P., Prange C., BL	BL	RT Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RA	Bosak S.A., Logue L.N.A., Peters G.J., Abramson R.D., Mullany S.J., DR	DR	DR EMBL; AK129787; BAC8225.1.
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W., DR	DR	DR EMBL; AK129787; BAC8225.1.
RA	Villarreal D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., SQ	Qy	Query Match Score 1225; DB 2; Length 470;
RA	Fahay J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,	Db	Best Local Similarity 97.0%; Pred. No. 2.7e-89; 3; Mismatches 4; Indels 0; Gaps 0;
RA	Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,	Qy	1 EPKSCDKTHTCPPCPAPELGGPSVLEPPKPKDTLMISRTPEVTCVVVDYSHEDPEVKF 60
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	Db	239 EPKSCDKTHTCPPCPAPELGGPSVLEPPKPKDTLMISRTPEVTCVVVDYSHEDPEVKF 298
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	Qy	61 NWYVGVEVHNVKTKPREEQNSTYRVSVLTILHQNQNGKEYCKVSNKALPPIKT 120
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,	Db	299 NWYVGVEVHNAKTQPREEQNSTYRVSVLTILHQDNLNGKEYCKVSNKALPPIKT 358
RA	Jones S.J., Marrs M.A.;	Qy	121 ISKAKVQPREPOVYTIPPSRDELTKNQVSLLTCLVKFQYSDIAVEWSNGOPENNYKTP 180
RT	"Generation and initial analysis of more than 15,000 full-length human	Db	359 ISKAKGQPREPOVYTIPPSRDELTKNQVSLLTCLVKFQYSDIAVEWSNGOPENNYKTP 418
RL	and mouse cDNA sequences";	RN	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	RP	SEQUENCE FROM N.A.
RL		RC	TISSUE=Spleen;
RL		RA	Strausberg R.I.
RL		RA	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR		RA	EMBL; BC05384; AAH5384.1.
DR		DR	InterPro; IPR07110; Ig-like.
DR		DR	InterPro; IPR03597; Ig-cl.
DR		DR	InterPro; IPR03006; Ig_MHC.
DR		DR	InterPro; IPR03096; Ig_V.
PFam		PFam	PF07654; C1-set; 3.
PFam		DR	PF00047; Ig_1.
DR		DR	SMART; SM00406; IgV; 1.
DR		DR	Search completed: October 27, 2004, 17:03:56

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ATTACHMENTS

~~maximum DB seq length: 200000000~~

SUMMARIES						
Result No.	Score	Query Match Length	DB	ID	%	Description
1	1260	100.0	232	6	AA019665	Aa01
2	1260	100.0	330	6	AA019664	Aa01
3	1260	100.0	569	6	AA019668	Aa01
4	1225	97.2	232	2	AABW2232	Aab2
5	1225	97.2	232	3	AABZ8690	Aab8
6	1225	97.2	232	4	AAB80897	Aay7
7	1225	97.2	232	4	AAY73915	Aae1
8	1225	97.2	232	5	AAE13347	Aae2
9	1225	97.2	232	5	AAB2272	Adj2
10	1225	97.2	232	7	ADJ65591	Adj5
11	1225	97.2	232	8	ADJ57512	Abb0
12	1225	97.2	233	5	ABB08463	Abj1
13	1225	97.2	235	6	ABJ38447	Ada8
14	1225	97.2	235	6	ADA89055	Add2
15	1225	97.2	235	7	ADD22647	Adg7
16	1225	97.2	235	7	ADG74307	Adg7
17	1225	97.2	247	5	AAE26774	Aee3
18	1225	97.2	251	5	ABB81490	Aab4
19	1225	97.2	251	6	AAE35154	Aar9
20	1225	97.2	259	2	AAY24154	Aay2
21	1225	97.2	267	5	AAE26773	Aae2
22	1225	97.2	269	5	ADJ52120	Adj5
23	1225	97.2	287	4	AAB47590	Aab4
24	1225	97.2	329	2	AAR91806	Aar9
25	1225	97.2	330	4	AAR04071	Aab0

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

1225	97.2	330	5	AAb478556	Human IgG
1225	97.2	330	5	AAb21960	Human IgG
1225	97.2	330	5	AAb81641	Human IgG
1225	97.2	330	5	AbbC07336	Human IgG
1225	97.2	330	5	AbbC07336	Human IgG
1225	97.2	330	6	Abp71856	Human IgG
1225	97.2	330	6	AAb332915	Human IgG
1225	97.2	330	6	AAb332915	Human IgG
1225	97.2	330	6	Aae32227	Human IgG
1225	97.2	330	6	AAb32227	Human IgG
1225	97.2	330	6	AAb8103	Human DR6
1225	97.2	330	6	Aao31102	Human A2
1225	97.2	330	6	Abp58336	Anti-Ang-
1225	97.2	330	6	Aao30893	Human IgG
1225	97.2	330	6	AAb30893	Human IgG
1225	97.2	330	7	Adf11389	Anti- <i>c</i> -PGL
1225	97.2	330	7	Adf67351	Human IgG
1225	97.2	330	7	Adf893605	Cytokine
1225	97.2	330	7	Adf575001	Human IgG
1225	97.2	330	8	Adm41537	Anti-inte-
1225	97.2	330	8	Adm68911	Human IgG
1225	97.2	330	8	Adn36570	Chemokine
1225	97.2	330	8	Adn973485	Artificial
1225	97.2	330	8	AAb91105	Human TR-
1225	97.2	330	8	AAb91105	Human TR-

LT 1
9665
AAO19665 standard; protein; 232 AA.

Human IgG1 heavy chain constant region hinge-CH2-CH3 portion.

Human; IgG1; immunoglobulin G; immunotherapy; immune disease;
Fc_{psilon}RI receptor; autoimmune disease; constant region; heavy chain;
antiasthmatic; anti-allergic; antiinflammatory; dermatological;
antiarthritic; antidiabetic; antirheumatic; neuroprotective;
hinge-CH2-CH3 region.

Homo sapiens.
 WO200288317-A2.
 07-NOV-2002.
 01-MAY-2002; 2002WO-US013527.
 01-MAY-2001; 2001US-00847208.
 24-OCT-2001; 2001US-00000439.
 (REGC) UNIV CALIFORNIA.

Saxon A, Zhang K, Zhu D;
 WPI; 2003-103456/09.

New fusion molecules comprising polypeptide sequences that bind to IgG inhibitory receptor and native IgE receptor, useful for treating IgE-mediated hypersensitivity reactions, e.g. asthma or allergies, or autoimmune diseases.

Claim 19; Fig 3; 116pp; English.

The present invention relates to a fusion molecule comprising a first polypeptide sequence capable of specific binding to a native IgG inhibitory receptor consisting of an immune receptor tyrosine-based inhibitory motif (ITIM), expressed on mast cells, basophils or B cells, functionally connected to a second polypeptide sequence capable of specific binding directly or indirectly to a native IgE receptor (IgEpsilonR). Also provided are nucleic acid sequences encoding such a fusion protein. The fusion molecules and compositions are useful for

treating an IgE-mediated biological response, preferably an IgE-mediated hypersensitivity reaction, such as asthma, allergic rhinitis, atopic dermatitis, severe food allergies, chronic urticaria, angioedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, type I diabetes mellitus, or multiple sclerosis, and for preventing of, or symptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present sequence is the human IgE1 heavy chain constant region hinge-CH2-CH3 portion

Query Match	Score 1260; DB 6; Length 23;		
Best Local Similarity 100.0% ; Pred. No. 2. 8e-1; Mismatches 0;保守性匹配 23;			
Matches 0; Insertions 0; Deletions 0; Gaps 0;			
1 EPKSCDKTHTCPPCPAPELGGSVFLFPPKPKDTMISRPEVTCVVVDVSHEDBEVKF 60			
1 EPKSCDKTHTCPPCPAPELGGSVFLFPPKPKDTMISRPEVTCVVVDVSHEDBEVKF 60			
61 NWYDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNMNGKEYKCKVSNKALPAPIKT 120			
61 NWYDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNMNGKEYKCKVSNKALPAPIKT 120			
121 ISKAXVQPRPQQVTLPPRDELTKNQSLTLCVKGTPSDIAVENESENOPENNYKTTP 180			
121 ISKAXVQPRPQQVTLPSRDELTKNQSLTLCVKGFYPSDIAVENESENOPENNYKTTP 180			
181 PVLDSVGSPFLYSLTVTDKSRQOGNVSCTYMEALTHNHYQRSILSLSPK 232			
181 PVLDSVGSPFLYSLTVTDKSRQOGNVSCTYMEALTHNHYQRSILSLSPK 232			

SUIT 2
D19664
AAO19664 standard, protein; 330 AA.

AAO19664;

28-MAR-2003 (first entry)

Human IgG1 heavy chain constant region.

Human; IgG1; immunoglobulin G; immunotherapy; immune disease;
Fc receptor; autoimmune disease; constant region; heavy chain;
antasthmatic; antiallergic; antiinflammatory; dermatological;
antiarthritic; antirheumatic; antidiabetic; neuroprotective.

Homo sapiens.

WO200288317-A2.

07-NOV-2002.

01-MAY-2002 / 2002WO-US013527.

01-MAY-2001: 2001US-00847208.

24-OCT-2001; 2001US-000000439.

(REGC) UNIV CALIFORNIA.

Saxon A., Zhang K., Zhu D.

WDT: 2003-103456/00

inhibitory receptor and native ICE receptor, useful for treating IGE-

הנִּזְמָן הַבָּשָׂר וְהַדְּבָרִים אֲשֶׁר־בָּאָתָּה

Query Match Similarity						
Best Local Matches		Score 1260; Pred. No. 4		Length 330;		
		0;	Mismatches	0;	Indels	Gaps
Qy	1	EPPSCDKTHTCPCKPCAPBLLGGPSVLFPPKPKDTLMSIRPEYTCVVVDVSHEDPEVKF	60			
Ds	99	EPPSCDKTHTCPCKPCAPBLLGGPSVLFPPKPKDTLMSIRPEYTCVVVDVSHEDPEVKF	150			
Qy	61	NWYVGVEVHNYTKPRBEQYNSTYRVSVLTVLHNQWNMNGKEYCKKVSNKALPAPIEKT	120			
Ds	159	NWYVGVEVHNYTKPRBEQYNSTYRVSVLTVLHNQWNMNGKEYCKKVSNKALPAPIEKT	210			
Qy	121	ISKAQKOPREPOYYTLPSSRDELTKNQSYSLTCLVKGSFYPSPDIAWESNQOPENNYKTP	180			
Ds	219	ISKAQKQPREFQVYTLPSSRDELTKNQSYSLTCLVKGSFYPSPDIAWESNQOPENNYKTP	270			
Qy	181	PVLDIVGSFFLYSKLTVDKSRMQLQGNVFSCSVMHEALHNHYQQRSLISPLCK	232			
Ds	279	PVLDIVGSFFLYSKLTVDKSRMQLQGNVFSCSVMHEALHNHYQQRSLISPLCK	330			

RESULT 3	
AAO19668	ID AAO19668 standard; protein; 569 AA.
XX	
AC	AAO19668;
XX	
DT	28-MAR-2003 (first entry)
XX	
DE	GB2 fusion protein for use in treating immune diseases.
XX	
KW	Human; IgE; immunoglobulin E; immunotherapy; immune dis-
Fc epsilon receptor; autoimmune disease; constant region	
KW	antiasthmatic; antiallergic; antiinflammatory; dermatoo-
KW	antiarthritic; antirheumatic; antidiabetic; neuroprotective
KW	fusion protein.

Synthetic	OS	01-MAY-2002;	2002WO-US01352
Unidentified.	XXX	01-MAY-2001;	2001US-US084720
	PN	PR	24 OCT 2001
	XX		24 OCT 2001
	PD	07-NOV-2002.	
	XX		
	XXX		

(REGC) UNIV CALIFORNIA.
Saxon A, Zhang K, Zhu D;
WPI: 2003-103456/09.

inhibitory receptor and native IgE receptor, useful for treating IgE-mediated hypersensitivity reactions, e.g. asthma or allergies, or autoimmune diseases.

Claim 35; Fig 7; 116pp; English.

The present invention relates to a fusion molecule comprising a first polypeptide sequence capable of specific binding to a native IgG inhibitory receptor consisting of an immune receptor tyrosine-based motif (ITIM), expressed on mast cells, basophils or B cells, functionally connected to a second polypeptide sequence capable of specific binding directly or indirectly to a native IgE receptor (PeptisonR). Also provided are nucleotide sequences encoding such a fusion protein. The fusion molecules and compositions are useful for treating an IgE-mediated biological response, preferably an IgE-mediated hypersensitivity reaction, such as asthma, allergic rhinitis, atopic dermatitis, severe food allergies, chronic urticaria, angioedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, type-I diabetes mellitus, or multiple sclerosis, and for preventing of, or symptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present sequence is a gamma-hinge-ChIgamm2a3-(Gly4Ser3-ChIpsilon3-ChIpsilon3) fusion protein (designated GB2) of the invention

Sequence 569 AA:

Query Match	100.0%	Score 1260;	DB 6;	Length 569;	
Best Local Similarity	100.0%;	Pred. No. 8.1e-91;			
Matches 232;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
)	1 EPKSCDKHTCPPOPAPAPLLGGPSVELFPPXPKDLMISRPETCTVYDVSHEDPEVKF 60				
)	1 EPKSCDKHTCPPOPAPAPLLGGPSVELFPPXPKDLMISRPETCTVYDVSHEDPEVKF 60				
)	61 NWYDGVEHNVTKPREEQYNSTYRVSVLTVLHQNMWNGKEYKCKVSNKALPAPIKT 120				
)	61 NWYDGVEHNVTKPREEQYNSTYRVSVLTVLHQNMWNGKEYKCKVSNKALPAPIKT 120				
)	121 ISKAKVQPREPVYTLPSPSRDLETLKNQVSLTCLVKGFPYPSDIAVENEWSQOPENNYKTP 180				
)	121 ISKAKVQPREPVYTLPSPSRDLETLKNQVSLTCLVKGFPYPSDIAVENEWSQOPENNYKTP 180				
)	181 PVLDIVSGSFPLYSLTVKDSRQOGNVSFCSCVMEALHNHYQQRSLSLSPGK 232				
)	181 PVLDIVSGSFPLYSLTVKDSRQOGNVSFCSCVMEALHNHYQQRSLSLSPGK 232				

RESULT 4

WZ26232 standard; protein; 232 AA.

{ AAN26232;

{ 16-MAR-1998 (first entry)

{ Human IgG1 hinge/Fc region.

{ Fusion protein; hydrophilic spacer; recombinant; expression system; carboxypeptidase; IgG1; immunoglobulin; hinge region; Pc.

{ Homo sapiens.

{ WO9728272-A1.

{ 07-AUG-1997.

{ 31-JUN-1997; 97WO-US001470.

{ 31-JUN-1996; 96US-00595043.

{ (TECH-) TECHNOLOGENE INC.

{ Sgarlato GD;

XX WPI; 1997-402624/37.

DR DR-PSDB; AAT80158.

XX

PT

PT

PT

PT

PT

PT

PT

PT

XX Recombinant protein expression system for fusion protein production - useful for high quality production of authentic recombinant proteins.

XX Example 3; Page 133-134; 194pp; English.

CC A novel recombinant vector has been developed which comprises a CC nucleotide sequence encoding a fusion protein. The fusion protein CC comprises three domains joined together in order, from N-terminus to C- CC terminus, of a first domain comprising a protein of interest, a second CC domain comprising a hydrophilic spacer and an affinity domain, each CC domain comprising amino acid residues. The present sequence represents CC the hinge/FC region of human IgG1, used in example 3 of the present CC invention. The recombinant vector is used for the production of authentic CC recombinant proteins of interest. The method of the invention is useful CC for the expression of fusion proteins capable of isolation by affinity CC chromatography in pro- or eukaryotic cells. This method allows for the CC efficient cleavage and generation of authentic proteins of interest that CC do not contain extraneous (i.e. non-naturally occurring) amino acids CC

XX

Sequence 232 AA:

Query Match	97.2%;	Score 1225;	DB 2;	Length 232;	
Best Local Similarity	97.0%;	Pred. No. 1.6e-88;			
Matches 225;	Conservative 3;	Mismatches 4;	Indels 0;	Gaps 0;	
)	1 EPKSCDKHTCPKPAPELGGPSVLFPPPKPDKTMISRTPEVTCVVDPSHDDPEVKF 60				
)	1 EPKSCDKHTCPKPAPELGGPSVLFPPPKPDKTMISRTPEVTCVVDPSHDDPEVKF 60				
)	61 NWYDGVEHNVTKPREEQYNSTYRVSVLTVLHQNMWNGKEYKCKVSNKALPAPIKT 120				
)	61 NWYDGVEHNVTKPREEQYNSTYRVSVLTVLHQNMWNGKEYKCKVSNKALPAPIKT 120				
)	121 ISKAKVQPREPVYTLPSPSRDLETLKNQVSLTCLVKGFPYPSDIAVENEWSQOPENNYKTP 180				
)	121 ISKAKVQPREPVYTLPSPSRDLETLKNQVSLTCLVKGFPYPSDIAVENEWSQOPENNYKTP 180				
)	181 PVLDIVSGSFPLYSLTVKDSRQOGNVSFCSCVMEALHNHYQQRSLSLSPGK 232				
)	181 PVLDIVSGSFPLYSLTVKDSRQOGNVSFCSCVMEALHNHYQQRSLSLSPGK 232				

RESULT 5

AAB28690

1D

AA28690 standard; protein; 232 AA.

XX

AAB28690;

AC

AA28690;

XX

14-FEB-2001 (first entry)

XX

DE

Human IgGammal hinge, CH2 and CH3 regions.

XX

KW Human; AGP-1; type II transmembrane protein; cytostatic; antiviral;

KW Human inflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV;

KW human immunodeficiency virus; apoptosis; proliferative disorder; cancer;

KW hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;

KW transplant rejection; cardiovascular disease; arteriosclerosis;

KW IgGammal.

XX

Homo sapiens.

XX

OS

WO200063253-A1.

XX

PD

26-OCT-2000.

XX

PF

24-MAR-2000; 2000WO-US008004.

XX

PR

16-APR-1999;

99US-00293245.

XX

PA	AMGEN INC.	XX	XX	PI	Dunstan CR;
PI		XX	XX	DR	
Hsu H.	Meng S.	XX	XX	WPI;	2001-265936/27.
DR		XX	XX	PT	Preventing or treating lytic bone diseases, particularly associated with cancer or metastasis, by administering an osteoprotegerin polypeptide.
WPI;	2000-665240/64.	XX	XX	PR	
PT	Fusion protein of AGP-1 protein and an FC region, used to treat proliferative disorders, immune disorders, and virally-induced disorders.	XX	XX	PS	Disclosure; Fig 1; 87pp; English.
PT	Claim 2; Fig 1; 93pp; English.	XX	XX	CC	The present invention relates to a method for the prevention or treatment of lytic bone disease or multiple myeloma. Also the method can be used for preventing metastasis of cancer to bone or osteosarcoma.
PS	The present sequence was used in the production of AGP-1 fusion proteins. AGP-1 is a type II transmembrane protein. The fusion proteins comprise an Fc immunoglobulin region fused to the N-terminal portion of the AGP-1 protein. The fusion proteins can be used to induce apoptosis in a tissue, and to treat proliferative disorders, immune disorders, or virally-induced disorders. The proliferative disorders include cancers, such as breast, prostate, lung or colon cancer. The viral infections include hepatitis, and acquired immunodeficiency syndrome (AIDS), and the immune disorders may be autoimmune disorders or transplant rejection.	XX	CC	CC	metastasis. The method comprises administering an OPG (osteoprotegerin) polypeptide or OPG fusion protein. The OPG proteins (see AB0888-AAB0905) can inhibit formation of osteoclasts (and thus bone resorption) by blocking differentiation from monocytes/macrophage precursors. The present sequence is the hinge, CH2 and CH3 regions of human IgG gamma 1.
SQ	Cardiovascular diseases such as arteriosclerosis may also be treated. The AGP-1 containing fusion Proteins have increased biological activity compared to the soluble AGP-1 Proteins used in prior art therapies.	XX	CC	CC	This sequence can be used to generate fusion proteins of OPG and immunoglobulin, for use in the present invention. The generated fusion proteins can exhibit increased circulating half-lives and slower clearance times, thereby providing a more sustained activity
SQ	Sequence 232 AA;	XX	CC	CC	Sequence 232 AA;
Query	97.2%; Score 1225; DB 3; Length 232;	DB	4;	Length	232;
Best Local Similarity	97.0%; Pred. No. 1..6-88;	Matches	225;	Conservative	Score 1225; Pred. No. 1..6-88;
Matches	3; Mismatches	4;	3;	Mismatches	97.0%; Best Local Similarity
Db	1 EPKSCDKTHCPCKPAPELIGGPSVFLFPKPKDTLMISRTPEVTCTVVYDVSHEDPVKF	Db	1 EPKSCDKTHCPCKPAPELIGGPSVFLFPKPKDTLMISRTPEVTCTVVYDVSHEDPVKF	Db	1 EPKSCDKTHCPCKPAPELIGGPSVFLFPKPKDTLMISRTPEVTCTVVYDVSHEDPVKF
Qy	60	60	60	60	60
Db	1 EPKSCDKTHCPCKPAPELIGGPSVFLFPKPKDTLMISRTPEVTCTVVYDVSHEDPVKF	Db	1 EPKSCDKTHCPCKPAPELIGGPSVFLFPKPKDTLMISRTPEVTCTVVYDVSHEDPVKF	Db	1 EPKSCDKTHCPCKPAPELIGGPSVFLFPKPKDTLMISRTPEVTCTVVYDVSHEDPVKF
Qy	60	60	60	60	60
Db	61 NWYVDGEVHNAKTKPREEQNSTYRVSVLTIVLHQNNNGKEYKCVSNKALPAPIKT	Db	61 NWYVDGEVHNAKTKPREEQNSTYRVSVLTIVLHQNNNGKEYKCVSNKALPAPIKT	Db	61 NWYVDGEVHNAKTKPREEQNSTYRVSVLTIVLHQNNNGKEYKCVSNKALPAPIKT
Qy	61	61	61	61	61
Db	61 NWYVDGEVHNAKTKPREEQNSTYRVSVLTIVLHQDNNGKEYKCVSNKALPAPIKT	Db	61 NWYVDGEVHNAKTKPREEQNSTYRVSVLTIVLHQDNNGKEYKCVSNKALPAPIKT	Db	61 NWYVDGEVHNAKTKPREEQNSTYRVSVLTIVLHQDNNGKEYKCVSNKALPAPIKT
Qy	120	120	120	120	120
Db	121 ISKAQKOPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWNSGPENNYKTP	Db	121 ISKAQKOPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWNSGPENNYKTP	Db	121 ISKAQKOPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWNSGPENNYKTP
Qy	180	180	180	180	180
Db	121 ISKAQKOPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWNSGPENNYKTP	Db	121 ISKAQKOPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWNSGPENNYKTP	Db	121 ISKAQKOPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWNSGPENNYKTP
Qy	180	180	180	180	180
Db	181 PVLDSGSFPEFLYSKLTVDKSRWQCNVFCSVMHEALTHHYQRSLSLSPGK	Db	181 PVLDSGSFPEFLYSKLTVDKSRWQCNVFCSVMHEALTHHYQRSLSLSPGK	Db	181 PVLDSGSFPEFLYSKLTVDKSRWQCNVFCSVMHEALTHHYQRSLSLSPGK
Qy	232	232	232	232	232
Db	232	232	232	232	232

Dunstan CR, Wooden SK, Mann MB;
WPI; 2001-244572/25.

Osteoprotegerin-FC protein fusions useful for treating bone loss caused by e.g. osteoporosis, Paget's disease and osteomyelitis.

Claim 3; Fig 1; 119pp; English.

The patent discloses fusion protein comprising human osteoprotegerin (OPG) protein fused by linker to human IgG1 FC portion. OPG negatively regulates formation of osteoclasts in vitro and in vivo. It blocks the differentiation of osteoclasts from monocyte or macrophage precursors and the reabsorption of bone. The OPG-FC fusion protein is administered for the treatment of bone loss resulting from osteoporosis, Paget's disease, osteomyelitis, hypercalcaemia, osteopenia associated with surgery or steroid administration, osteonecrosis, bone loss due to rheumatoid arthritis, periodontal bone loss, osteolitic metastasis and/or prosthetic loosening. The present sequence is human immunoglobulin G (Ig G) constant heavy chain (CH2, CH3) hinge and heavy chain constant regions CH2 and CH3 protein comprising the hinge and heavy chain constant regions CH2 and CH3.

Sequence 232 AA;

	Query Match	Match	Score	Length	DB	5;	Length
	Best Local Similarity	97.2%	Score 1225;	Length 232;			
	Matches	97.0%;	Pred. No. 1.6e-88;				
	225; Conservative	3;	Mismatches 4;	Indels 0;	Gaps 0;		
/	1	EPKSDDKTHCPCKPAPELLGGPSVFLPPKPKDTLMISRPEVTCVVDVSHEPDPEVKF	60		Qy	1	EPKSDDKTHCPCKPAPELLGGPSVFLPPKPKDTLMISRPEVTCVVDVSHEPDPEVKF 60
/	1	EPKSDDKTHCPCKPAPELLGGPSVFLPPKPKDTLMISRPEVTCVVDVSHEPDPEVKF	60		Db	1	EPKSDDKTHCPCKPAPELLGGPSVFLPPKPKDTLMISRPEVTCVVDVSHEPDPEVKF 60
/	61	NWYTDGVVEHVNVIKTPREEQYNSTYRVVSLTVLHQNMNGKEYKCKVSNKALPAPIKT	120		Qy	61	NWYTDGVVEHVNVIKTPREEQYNSTYRVVSLTVLHQNMNGKEYKCKVSNKALPAPIKT 120
/	61	NWYTDGVVEHVNVIKTPREEQYNSTYRVVSLTVLHQDWLNGEYKKCKVSNKALPAPIKT	120		Db	61	NWYTDGVVEHVNVIKTPREEQYNSTYRVVSLTVLHQDWLNGEYKKCKVSNKALPAPIKT 120
/	121	ISAKVQPREPVQYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWSNGOPENNYKTP	180		Qy	121	ISAKVQPREPVQYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWSNGOPENNYKTP 180
/	121	ISAKVQPREPVQYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWSNGOPENNYKTP	180		Db	121	ISAKVQPREPVQYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWSNGOPENNYKTP 180
/	181	PVLDSVGSEFLSKLTVTDSRQOGNVPFSCSVMHEALTHNHYQQLSLSPK	232		Qy	181	PVLDSVGSEFLSKLTVTDSRQOGNVPFSCSVMHEALTHNHYQQLSLSPK 232
/	181	PVLDSGSEFLSKLTVTDSRQOGNVPFSCSVMHEALTHNHYQQLSLSPK	232		Db	181	PVLDSGSEFLSKLTVTDSRQOGNVPFSCSVMHEALTHNHYQQLSLSPK 232

RESULT 8

AAE15347 standard; protein; 232 AA.

AAE15347;

09-APR-2002 (first entry)

Human immunoglobulin G (IgG) gamma 1 constant heavy chain hinge region.
Human; erythropoietin; Epo; haematoцит; anaemia; kidney function; Igs;
cancer; myelosuppressive therapy; anti-viral drug; immunoglobulin G.
Homo sapiens.

WO200181405-A2.
01-NOV-2001.

X F 19-APR-2001; 2001WO-US012836.
X R 21-APR-2000; 2000US-00559001.

X (AMGE-) AMGEN INC.

I Egrie JC, Elliott SG, Browne JK, Sitney KC;

DR WPI; 2002-034433/04.

XX PT Increasing and maintaining hematocrit in mammal suffering from anemia, PT comprising administering hyperglycosylated analog of erythropoietin less PT frequently and at lower molar amount of recombinant human erythropoietin. XX

PS Example 1; Fig 10; 95pp; English.

CC The invention relates to a method for increasing and maintaining a CC haematocrit in a mammal. The method comprises administering a pharmaceutical CC hyperglycosylated analogue of erythropoietin (Epo) in a pharmaceutical composition, less frequently than an equivalent molar amount of and at a CC lower molar amount than recombinant human Epo (rHuEpo) to obtain a comparable target hematocrit. Epo is a Glycoprotein hormone necessary CC for the maturation of erythroid Progenitor cells into erythrocytes. Human CC Epo analogue is useful for raising and maintaining hematocrit to a comparable target hematocrit in a mammal suffering from anaemia CC associated with a decline or loss of kidney function, myelosuppressive CC therapy comprising chemotherapeutic or anti-viral drugs or associated CC with excessive blood loss during surgical procedures, and in cancer CC condition. The present sequence is human immunoglobulin G (IgG) Gamma 1 CC constant heavy chain (CH2, CH3) hinge region used to construct Epo CC hyperglycosylated analogue fusion protein.

XX Sequence 232 AA;

	Query Match	Match	Score	Length	DB	5;	Length
	Best Local Similarity	97.2%	Score 1225;	Length 232;			
	Matches	97.0%;	Pred. No. 1.6e-88;				
	225; Conservative	3;	Mismatches 4;	Indels 0;	Gaps 0;		
/	1	EPKSDDKTHCPCKPAPELLGGPSVFLPPKPKDTLMISRPEVTCVVDVSHEPDPEVKF	60		Qy	1	EPKSDDKTHCPCKPAPELLGGPSVFLPPKPKDTLMISRPEVTCVVDVSHEPDPEVKF 60
/	1	EPKSDDKTHCPCKPAPELLGGPSVFLPPKPKDTLMISRPEVTCVVDVSHEPDPEVKF	60		Db	1	EPKSDDKTHCPCKPAPELLGGPSVFLPPKPKDTLMISRPEVTCVVDVSHEPDPEVKF 60
/	61	NWYTDGVVEHVNVIKTPREEQYNSTYRVVSLTVLHQNMNGKEYKCKVSNKALPAPIKT	120		Qy	61	NWYTDGVVEHVNVIKTPREEQYNSTYRVVSLTVLHQNMNGKEYKCKVSNKALPAPIKT 120
/	61	NWYTDGVVEHVNVIKTPREEQYNSTYRVVSLTVLHQDWLNGEYKKCKVSNKALPAPIKT	120		Db	61	NWYTDGVVEHVNVIKTPREEQYNSTYRVVSLTVLHQDWLNGEYKKCKVSNKALPAPIKT 120
/	121	ISAKVQPREPVQYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWSNGOPENNYKTP	180		Qy	121	ISAKVQPREPVQYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWSNGOPENNYKTP 180
/	121	ISAKVQPREPVQYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWSNGOPENNYKTP	180		Db	121	ISAKVQPREPVQYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWSNGOPENNYKTP 180
/	181	PVLDSVGSEFLSKLTVTDSRQOGNVPFSCSVMHEALTHNHYQQLSLSPK	232		Qy	181	PVLDSVGSEFLSKLTVTDSRQOGNVPFSCSVMHEALTHNHYQQLSLSPK 232
/	181	PVLDSGSEFLSKLTVTDSRQOGNVPFSCSVMHEALTHNHYQQLSLSPK	232		Db	181	PVLDSGSEFLSKLTVTDSRQOGNVPFSCSVMHEALTHNHYQQLSLSPK 232

RESULT 9

AAE26272

ID AAE26272 standard; protein; 232 AA.

XX AC AAE26272;

XX DT 14-NOV-2002 (first entry)

XX DE Human IgG1 heavy chain.

XX Human; amyloidogenic protein; Alzheimer's disease; Huntington's disease; KW spongiform encephalopathy; familial amyloid cardiomyopathy; amyloidosis; KW Gerstmann-Straussler-Scheinker syndrome; spongiform encephalopathy; GSS; KW Creutzfeldt-Jacob disease; insulinoma; diabetes; body myocytis; myeloma; CJ.

KW Homo sapiens.

XX OS Homo sapiens.

XX PN WO200242462-A2.

XX PD 30-MAY-2002.

XX PF 27-NOV-2001; 2001WO-US044581.

XX PR 27-NOV-2000; 2000US-0253302P.

XX PR 29-NOV-2000; 2000US-0250198P.

3 Homo sapiens.
 4 WO2004005962-A2.
 5 22-JAN-2004.
 6 09-JUL-2003; 2003WO-DK00481.
 7 12-JUL-2002; 2002DK-00001099.
 8 (NOVO) NOVO NORDISK AS.
 9 Bjorn SE, Nicolaisen EM, Steensstrup TD;
 10 WPI; 2004-180224/17.
 11 New compound binding to tissue factor, useful for treating diseases such
 12 as angiogenesis, ischemia/reperfusion, and rheumatoid arthritis.
 13 Claim 16; SEQ ID NO 7; 61pp; English.
 14 The invention relates to a compound (I) binding to tissue factor (TF).
 15 The compound (I) has the formula A-(LM)-C, where A is a FVIIa
 16 polypeptide, LM is an optional linker group, C comprises an
 17 immunostimulatory effector domain, and (I) binds to TF. (I) inhibits TF-
 18 mediated activated factor VII (FVIIa) activity. (I) is useful as a
 19 medicament, and for the manufacture of a medicament for preventing or
 20 treating disease or disorder associated with pathophysiological TF
 21 activity. The disease or disorder associated with pathophysiological TF
 22 activity are deep venous thrombosis, arterial thrombosis, post surgical
 23 thrombosis, coronary artery bypass graft (CABG), percutaneous transdermal
 24 coronary angioplasty (PTCA), stroke, cancer, tumor metastasis,
 25 angiogenesis, ischemia/reperfusion, rheumatoid arthritis, thrombolytic,
 26 arteriosclerosis and restenosis following angioplasty, acute and chronic
 27 indications such as inflammation, septic shock, septicemia, hypertension,
 28 adult respiratory distress syndrome (ARDS), disseminated intravascular
 29 coagulopathy (DIC), pulmonary embolism, platelet deposition, myocardial
 30 infarction, or prophylactic treatment of mammals with atherosclerotic
 31 vessels at risk for thrombosis. The present sequence represents the Fc
 32 domain fragment of human immunoglobulin G1 (IgG1).
 33 Sequence 232 AA;
 34 Query Match Score 1225; DB 8; Length 232;
 35 Best Local Similarity 97.0%; Pred. No. 1_6e-88;
 36 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 37 Y 1 EPKSCDKTHCPCCPAPELGGPSVFLPPPKPKDTLMISRQDPEVKF 60
 38 b 1 EPKSCDKTHCPCCPAPELGGPSVFLPPPKPKDTLMISRQDPEVKF 60
 39 Y 61 NWYDGVEHNWKTKEPREQYNSTYRVSVLTVLHQNMNGKEYKCKVSNKALPAPIKT 120
 40 b 61 NWYDGVEHNWKTKEPREQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIKT 120
 41 Y 121 ISKAKVQPREPQYTLPPSRDELTKQVSLTUVKCFYPSDIAVEMESNGOPENNYKTTP 180
 42 b 121 ISKAKVQPREPQYTLPPSRDELTKQVSLTUVKCFYPSDIAVEMESNGOPENNYKTTP 180
 43 Y 181 PVLDVGSGFFLYSLTVDSRWRQQNVFSCSVMEEAHNHYQTSLSLSPGK 232
 44 b 181 PVLDVGSGFFLYSLTVDSRWRQQNVFSCSVMEEAHNHYQTSLSLSPGK 232
 45 E RESULT 12
 46 BBC09463 Standard; protein; 233 AA.
 47 X AB09463;
 48 C AB09463;
 49 T 01-JUL-2002 (first entry)
 50 X Human IgG Fc fragment amino acid sequence.

51 XX Protein A; immunoglobulin G; IgG; antibody; human.
 52 KW XX
 53 OS XX
 54 Homo sapiens.
 55 PH XX
 56 Key Location/Qualifiers
 57 PT Misc-difference 168 /note= "encoded by GAC"
 58 FT Misc-difference 169 /note= "encoded by ACC"
 59 FT XX
 60 WO200204602-A1.
 61 PN XX
 62 PD 17-JAN-2002.
 63 XX 04-JUL-2001; 2001WO-JP005788.
 64 PF XX
 65 PR 07-JUL-2000; 2000JP-00206689.
 66 PA XX
 67 PI Tanaka A, Ueda M, Teranishi Y;
 68 XX DR WPI; 2002-180174/19.
 69 DR N-PSDB; ABUS2834.
 70 XX Transform yeast for stable supply of highly active catalytic antibody.
 71 PT PT comprises the capability of expressing and presenting protein A or its
 72 PT fragment, particularly with the Z2 domain, on the cell surface.
 73 XX PS Example 3; Fig 4; 25pp; Japanese.
 74 CC The invention relates to a transformant yeast that can present protein A
 75 CC or its fragment on its cell surface. The yeast can be used for detecting
 76 CC or isolating the Fc part of immunoglobulin (Ig)G. The yeast is useful for
 77 CC a stable supply of highly active catalytic antibody e.g. by screening
 78 CC novel functional molecules and in isolating Fc-carrying secretory
 79 CC proteins. The yeast of the invention is capable of adhering specifically
 80 CC to a combinatorial antibody library with an Fc-carrying antibody
 81 CC component. The current sequence represents the human IgG Fc fragment
 82 CC amino acid sequence
 83 XX Sequence 233 AA;
 84 SQ Query Match Score 1225; DB 5; Length 233;
 85 Best Local Similarity 97.0%; Pred. No. 1_6e-88;
 86 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 87 Y 1 EPKSCDKTHCPCCPAPELGGPSVFLPPPKPKDTLMISRQDPEVKF 60
 88 b 2 EPKSCDKTHCPCCPAPELGGPSVFLPPPKPKDTLMISRQDPEVKF 61
 89 Y 61 NWYDGVEHNWKTKEPREQYNSTYRVSVLTVLHQNMNGKEYKCKVSNKALPAPIKT 120
 90 b 62 NWYDGVEHNWKTKEPREQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIKT 121
 91 Y 121 ISKAKVQPREPQYTLPPSRDELTKQVSLTUVKCFYPSDIAVEMESNGOPENNYKTTP 180
 92 b 122 ISKAKVQPREPQYTLPPSRDELTKQVSLTUVKCFYPSDIAVEMESNGOPENNYKTTP 181
 93 Y 181 PVLDVGSGFFLYSLTVDSRWRQQNVFSCSVMEEAHNHYQTSLSLSPGK 232
 94 b 182 PVLDVGSGFFLYSLTVDSRWRQQNVFSCSVMEEAHNHYQTSLSLSPGK 233
 95 E RESULT 13
 96 ABJ38647 ID ABJ38647 standard; protein; 233 AA.
 97 XX AC
 98 XX DT 26-JUN-2003 (first entry)
 99 XX

DE	pcXFC protein SEQ ID No 6.	RESULT 14 ADA89055 ID ADA89055 standard; protein; 235 AA. XX	
XX	Cystostatic; osteopathic; cerebroprotective; dermatological; enzyme;	KW	
KW	antigen binding; receptor protein tyrosine kinase; skeletal dysplasia;	KW	
KW	constitutive activation; craniotarsal synostosis; cell proliferative disorder;	KW	
KW	achondroplasia; thanatophoric dysplasia; acanthosis nigricans dysplasia;	KW	
KW	hypochondroplasia; severe achondroplasia; transitional cell carcinoma;	KW	
KW	Muenke coronal craniosynostosis; Crouzon syndrome; acanthosis nigricans;	KW	
KW	tumour progression; osteosarcoma; chondrosarcoma; multiple myeloma;	KW	
KW	mammary carcinoma; fibroblast growth factor receptor 3; FGFR3 protein.	KW	
XX	Homo sapiens.	OS	
OS	XX	antigen binding; antibody; specific binding affinity;	
PN	WO2002102854-A2.	PN	
XX	XX	KW receptor protein tyrosine kinase; RPTK;	
PD	27-DEC-2002.	XX	KW receptor protein tyrosine kinase inhibitor;
XX	XX	KW fibroblast growth factor receptor; FGFR; osteopathic; cytostatic;	
PF	20-JUN-2002; 2002WO-1B003523.	XX	KW ophthalmological; bone disorder; cartilage disorder; skeletal disorder;
XX	XX	KW skeletal dysplasia; achondroplasia; thanatophoric dysplasia;	
PR	20-JUN-2001; 2001US-0299187P.	XX	KW hypochondroplasia; craniotarsal synostosis disorder;
PA	(MORP-) MORPHOSYS AG.	XX	KW malignant cell proliferation disease; cancer; tumour; vision disorder;
PA	(PROC-) PROCHON BIOTECH LTD.	XX	KW non-neoplastic angiogenic pathologic condition.
PA	XX	OS Synthetic.	
PI	Thomassen-Wolf, B., Borges, E., Rayon, A., Rom, E.;	OS Homo sapiens.	
XX	XX	XX PN WO2002102973-A2.	
DR	WPI; 2003-167489/16.	XX	
DR	N-PSDB; ABT40262.	PD 27-DEC-2002.	
XX	New molecules having the antigen-binding portion of antibodies that block	XX	
PT	activation of receptor protein tyrosine kinase, useful for treating or	PT 20-JUN-2002; 2002WO-1L000495.	
PT	inhibiting skeletal dysplasias, craniotarsal synostosis or cell proliferative	XX PR 20-JUN-2001; 2001US-0299187P.	
PT	disorders.	XX PA (PROC-) PROCHON BIOTECH LTD.	
PS	Example 2; Page 38; 103pp; English.	XX PA	
XX	The invention relates to a novel molecule comprising the antigen binding	XX PI Yaron, A., Rom, E;	
CC	portion of an isolated antibody, which has an increased affinity for a	XX DR WPI; 2003-173236/17.	
CC	receptor protein tyrosine kinase and which blocks constitutive activation	XX N-PSDB; ADA89054.	
CC	of the receptor protein tyrosine kinase. The methods and compositions of	XX	
CC	the invention are useful for treating or inhibiting a skeletal dysplasia,	PT New antibodies which have specific binding affinity for a receptor	
CC	craniotarsal synostosis or a cell proliferative disorder. The skeletal dysplasia	PT protein tyrosine kinase (RPTK) and block constitutive activation of RPTK,	
CC	is achondroplasia, thanatophoric dysplasia, hypochondroplasia, severe	PT useful for treating bone and cartilage disorders, or malignant cell	
CC	achondroplasia with developmental delay or acanthosis nigricans	PT proliferative diseases.	
CC	CC	CC Example 2; Page 43; 122pp; English.	
CC	CC	CC The present invention describes molecule (1) comprising the antigen	
CC	CC	CC binding portion of an isolated antibody which has specific binding	
CC	CC	CC affinity for a receptor protein tyrosine kinase (RPTK), particularly for	
CC	CC	CC a fibroblast growth factor receptor (FGFR), and which blocks constitutive	
CC	CC	CC activation of an RPTK. Also described: (1) pharmaceutical compositions	
CC	CC	CC comprising (1) as an active ingredient and a pharmaceutical carrier,	
CC	CC	CC excipient, or auxiliary agent; (2) a kit comprising (1), at least one	
CC	CC	CC reagent for detecting the presence of (1) when bound to the RPTK, and	
CC	CC	CC instructions for use; (3) a method for treatment of bone and cartilage	
CC	CC	CC related disorders by administering a composition of (1) to the subject;	
CC	CC	CC (4) a method for treating or inhibiting a cell proliferative disease or	
CC	CC	CC disorder by administering the composition of (1); (5) a method for	
CC	CC	CC screening a molecule comprising the antigen-binding portion of an	
CC	CC	CC antibody which blocks ligand-dependent activation of RPTK; (6) an	
CC	CC	CC isolated nucleic acid molecule encoding a VL-CDR3 DNA region and a VH-	
CC	CC	CC CDR3 DNA region; (7) an isolated nucleic acid molecule encoding VL region	
CC	CC	CC and a VH region; (8) vectors comprising a nucleic acid molecule of (6) or	
CC	CC	CC (7); and (9) host cells transformed with the vector. (1) have	
CC	CC	CC osteopathic, cytostatic and ophthalmological activities, and can be used	
CC	CC	CC as a RPTK inhibitor. Compositions comprising (1) are useful for treating	
CC	CC	CC bone and cartilage disorders, including skeletal disorders such as	
CC	CC	CC skeletal dysplasia (achondroplasia, thanatophoric dysplasia, delay and	
CC	CC	CC hypochondroplasia, severe achondroplasia with developmental delay and	
CC	CC	CC acanthosis nigricans dysplasia) or a craniotarsal synostosis disorder (e.g.	
CC	CC	CC Muenke coronal craniotarsal synostosis or Crouzon syndrome with acanthosis	
CC	CC	CC nigricans). The composition may also be used for treating or inhibiting	
SQ	Sequence 235 AA;	Query Match 97.2%; Score 1225; DB 6; Length 235;	
	Best Local Similarity 97.0%; Pred. No. 1..6-88; Indels 0; Gaps 0;	Matches 225; Conservative 3; Mismatches 4;	
Qy	1 EPKSCDTHTCPPCPAPELGGPSVSLTPKREEQINSTYRVVSYLTVLHQNNNGKEYKCVSNKALPAPLKKT	60	
Db	4 EKXSCDTHTCPPCPAPELGGPSVSLTPKREEQINSTYRVVSYLTVLHQNNNGKEYKCVSNKALPAPLKKT	63	
Qy	61 NWYVGVEHNVKTKPREEQINSTYRVVSYLTVLHQNNNGKEYKCVSNKALPAPLKKT	120	
Db	64 NWYVGVEHNVAKTKPREEQINSTYRVVSYLTVLHQDLWINGKEYKCVSNKALPAPLKKT	123	
Qy	121 ISKAKTYPREPOVYIPLPSRDELTKVQSLTCLYKGFYPSDIAVEMESNGOPENNYTTP	180	
Db	124 ISKAKGPREPVYIPLPSRDELTKVQSLTCLYKGFYPSDIAVEMESNGOPENNYTTP	183	
Qy	181 PVLDSGSEFLYSLKLTVDKSRWQGNTVFSCSVMHEALHNHYQQRSLSPGK	232	
Db	184 PVLDSGSEFLYSLKLTVDKSRWQGNTVFSCSVMHEALHNHYTQSLSPGK	235	

malignant cell proliferative disease or disorder associated with abnormal RPTK activity, including a haemopoietic malignancy (e.g. multiple myeloma), solid tumours (e.g. mammary, colon, cervical, bladder, colorectal, chondrosarcoma or osteosarcoma), tumour formation, primary tumours, tumour progression (particularly progression of transitional cell carcinoma or mammary carcinoma), or tumour metastasis, where the cell proliferative disorder may be associated with the action of a constitutively activated RPTK, or with ligand-dependent activation of RPTK. The compositions may further be used for treating hyperproliferative diseases and disorders associated with ligand-dependent FGFR signalling, such as vision disorders (e.g. neovascular glaucoma, macular degeneration and proliferative retinopathy including diabetic retinopathy), and non-neoplastic angiogenic pathologic conditions (e.g. haemangiomas, angiofibromas and psoriasis). The present sequence is given in the exemplification of the present invention.

Sequence 235 AA;

Query Match	97.2%	Score 1225;	DB 6;	Length 235;
Best Local Similarity	97.0%	Pred. No. 1	6-88;	
Matches 225;	Conservative	3;	Mismatches 4;	Indels 0;
Gaps 0;				

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1 EPKSCDKTHCPPAPAPLGGPAPVLEPPPKPDITLMSIRTPETVTVVDYSHEDDEVKF 60
4 EPKSCDKTHCPPAPAPLGGPAPVLEPPPKPDITLMSIRTPETVTVVDYSHEDDEVKF 63
61 NWYDGVEHNVKTKPREQYNSTYRVSILVKCCKVSNKALPAPIEKT 120
64 NWYDGVEHNVAKTKPREQYNSTYRVSILVKCCKVSNKALPAPIEKT 123
121 ISKAQVQPREQYVTLPPSRDELTKNQSLTLCVKGYPSPDIAVENESNGOPENNYKTTP 180
124 ISKAQCPREQYVTLPPSRDELTKNQSLTLCVKGYPSPDIAVENESNGOPENNYKTTP 183
181 PVLDGSFPLYSKLTVDKSRWQGNVSCSYNHEALHNHYQSLSPGK 232
3 184 PVLDGSFPLYSKLTVDKSRWQGNVSCSYNHEALHNHYQSLSPGK 235

```

RESULT 15

D22647 standard; protein; 235 AA.

ADD25647;

X 15-JAN-2004 (first entry)

E Binding domain-immunoglobulin fusion protein-associated protein #101.
W Binding domain; immunoglobulin; fusion protein; cytosatic;
W antiarthritic; immunosuppressive; antidiabetic;
W neuroprotective; hinge region; immunoglobulin heavy chain;
W antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
W rheumatoid arthritis; myasthenia gravis; Grave's disease;
W type I diabetes mellitus; multiple sclerosis; autoimmune disease;
S Unidentified.

X US2003118592-A1.

X 26-JUN-2003.

X 25-JUL-2002; 2002US-00207655.

X X

X 17-JAN-2001; 2001US-0367358P.

R 17-JAN-2003; 2002US-0054530.

R 03-JUN-2002; 2002US-0385691P.

A (GENE-) GENECRAFT INC.

X Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;

XX WPI; 2003-801317/75.

DR New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.

XX Disclosure; SEQ ID NO 208; 15pp; English.

The invention relates to a binding domain-immunoglobulin fusion protein comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain CH2 constant region polypeptide that is fused to the hinge region polypeptide, and an immunoglobulin heavy chain CH3 constant region polypeptide that is fused to the CH2 constant region polypeptide. The hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; (b) where the mutated human IgG1 immunoglobulin hinge region polypeptide contains 2 cysteine residues, where the first cysteine is not mutated; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no more than one cysteine residue; and a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain-immunoglobulin fusion protein is capable of at least one immunological activity comprising antibody dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The binding domain polypeptide is capable of specifically binding to an antigen. Also included are an isolated polynucleotide encoding the binding domain-immunoglobulin fusion protein, recombinant expression construct comprising the polynucleotide (operably linked to a promoter), a host cell transformed or transfected with a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein, a pharmaceutical composition comprising the binding domain-immunoglobulin fusion protein or polynucleotide or a carrier, and treating a subject having or suspected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis, myasthenia gravis, type I diabetes mellitus, multiple sclerosis or autoimmune disease. The present sequence is a binding domain -immunoglobulin fusion protein-associated protein sequence. Note: The sequence data for this patent formed part of the printed specification and is also available in electronic format directly from USPTO at seqdata.uspto.gov/sequence.htm?DocID=20030118592. The authors have not identified the sequences in the printed specification by their SEQ ID number therefore none of the sequences can be explicitly identified.

XX Sequence 235 AA;

Query Match 97.2%; Score 1225; DB 7; Length 235;
Best Local Similarity 97.0%; Pred. No. 1 6-88;
Matches 225; Conservative 3; Mismatches 4; Indels 0;
Gaps 0;

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Qy	61 NWYDGVEHNVKTKPREQYNSTYRVSILVKCCKVSNKALPAPIEKT 120	Db	64 NWYDGVEHNVAKTKPREQYNSTYRVSILVKCCKVSNKALPAPIEKT 123
Qy	121 ISKAQVQPREQYVTLPPSRDELTKNQSLTLCVKGYPSPDIAVENESNGOPENNYKTTP 180	Db	124 ISKAQCPREQYVTLPPSRDELTKNQSLTLCVKGYPSPDIAVENESNGOPENNYKTTP 183
Qy	181 PVLDGSFPLYSKLTVDKSRWQGNVSCSYNHEALHNHYQSLSPGK 232	Db	184 PVLDGSFPLYSKLTVDKSRWQGNVSCSYNHEALHNHYQSLSPGK 235
Qy	121 ISKAQVQPREQYVTLPPSRDELTKNQSLTLCVKGYPSPDIAVENESNGOPENNYKTTP 180	Db	124 ISKAQGPREQYVTLPPSRDELTKNQSLTLCVKGYPSPDIAVENESNGOPENNYKTTP 183
Qy	181 PVLDGSFPLYSKLTVDKSRWQGNVSCSYNHEALHNHYQSLSPGK 232	Db	184 PVLDGSFPLYSKLTVDKSRWQGNVSCSYNHEALHNHYQSLSPGK 235

Thu Oct 28 05:36:46 2004

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Page 10

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SUMMARIES

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2	1260	100.0	232	14 US-10-000-439-3	Sequence 3, Appli
3	1260	100.0	330	10 US-09-847-208-2	Sequence 2, Appli
4	1260	100.0	330	14 US-10-000-439-2	Sequence 2, Appli
5	1260	100.0	569	10 US-19-847-208-7	Sequence 7, Appli
6	1260	100.0	569	14 US-10-000-439-7	Sequence 7, Appli
7	1225	92.2	232	9 US-09-996-357-10	Sequence 10, Appli
8	1225	97.2	232	10 US-19-389-782-1	Sequence 1, Appli
9	1225	97.2	232	16 US-10-617-619-7	Sequence 7, Appli
10	1225	97.2	235	16 US-10-761-593-26	Sequence 26, Appli
11	1225	97.2	235	14 US-10-207-655-208	Sequence 208, Appli
12	1225	97.2	247	9 US-09-996-357-13	Sequence 13, Appli
13	1225	97.2	251	14 US-10-008-063-18	Sequence 18, Appli

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; Sequence 3, Application US/09847208					
; GENERAL INFORMATION:					
; APPLICANT: Saxon, Andrew					
; APPLICANT: Zhang, Ke					
; APPLICANT: Zhu, Daocheng					
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF					
; FILE REFERENCE: UCC7-002A					
; CURRENT APPLICATION NUMBER: US/09/847,208					
; NUMBER OF SEQ ID NOS: 177					
; SOFTWARE: FastSEQ for Windows Version 4.0					
; SEQ ID NO 3					
; LENGTH: 232					
; TYPE: PRT					
; ORGANISM: Homo sapiens					
US-09-847-208-3					

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3	EPKSDDKTHCPPCAPELLGGPSVFLPPPKPDKTLMISRTPEVTCVVYDVSHEDPEVKF	60			
4	EPKSDDKTHCPPCAPELLGGPSVFLPPPKPDKTLMISRTPEVTCVVYDVSHEDPEVKF	60			
5	EPKSDDKTHCPPCAPELLGGPSVFLPPPKPDKTLMISRTPEVTCVVYDVSHEDPEVKF	60			
6	NWYDGVEVNNTKTPREQNNTYRVSVLTVLHQWNNGKEYCKVSNAKLPAPIKT	120			
7	NWYDGVEVNNTKTPREQNNTYRVSVLTVLHQWNNGKEYCKVSNAKLPAPIKT	120			
8	NWYDGVEVNNTKTPREQNNTYRVSVLTVLHQWNNGKEYCKVSNAKLPAPIKT	120			
9	NWYDGVEVNNTKTPREQNNTYRVSVLTVLHQWNNGKEYCKVSNAKLPAPIKT	120			
10	NWYDGVEVNNTKTPREQNNTYRVSVLTVLHQWNNGKEYCKVSNAKLPAPIKT	120			
11	ISAKVQPREPVQYTLPPSRDLTKQVSLLCLVGFYPSDIAVEWESNGOPENNYKTP	180			
12	ISAKVQPREPVQYTLPPSRDLTKQVSLLCLVGFYPSDIAVEWESNGOPENNYKTP	180			
13	ISAKVQPREPVQYTLPPSRDLTKQVSLLCLVGFYPSDIAVEWESNGOPENNYKTP	180			

TITLE OF INVENTION: Fc fusion Proteins of human erythropoietin with high biological
TITLE OF INVENTION: activities
FILE REFERENCE: Q2SUND001-A
CURRENT APPLICATION NUMBER: US/10/761,593A
CURRENT FILING DATE: 2004-01-21
PRIOR APPLICATION NUMBER: 09/928112
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.2
SEQ ID NO: 26
LENGTH: 232
TYPE: PRT
ORGANISM: Homo sapiens
IS-10761-593A-25

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Query Match      97.2%; Score: 1225;  DB: 90;  Length: 232;
Best Local Similarity 97.0%; Pred. No. 6.1e-90;
Matches 225;  Conservative 3;  Mismatches 4;  Indels 0;  Gaps 0;

Qy   1 EPKSCDKHTCPPCPAPELLGGPSVLFPPPKPKDTIMISRTPEVTYVVDVSHEDEPEYKF 60
    1 EPKSCDKHTCPPCPAPELLGGPSVLFPPPKPKDTIMISRTPEVTYVVDVSHEDEPEYKF 60
Db   61 NWYDGVVEHNVTKTPREEQYNSTYRVSVLTVLHQWNANGKEYKCKVSNKALPAPIEKT 120
    61 NWYDGVVEHNVTKTPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
Db   121 ISXKVKQREPQVTLPSSRDELTKNQVSITCLVKGFPSPDIAVWESNGOPENNYKTP 180
    121 ISXKVKQREPQVTLPSSRDELTKNQVSITCLVKGFPSPDIAVWESNGOPENNYKTP 180
Qy   181 PVLDSVGSSFLFLYSKLTVDKSRWQOGNFVFSVYMEALHNHYQQRSLSLSPGK 232
Db   181 PVLDSGSSFLFLYSKLTVDKSRWQOGNFVFSVYMEALHNHYTQSSLSLSPGK 232
Db   181 PVLDSGSSFLFLYSKLTVDKSRWQOGNFVFSVYMEALHNHYTQSSLSLSPGK 232

RESULT 11
US-10-2017-655-208
; Sequence 208 Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Leebetter, Jeffrey A.
; APPLICANT: Hayden-Leebetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069_401C1
; CURRENT APPLICATION NUMBER: US/10/2017 655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 208
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion polypeptide
US-10-2017-655-208

Query Match      97.2%; Score: 1225;  DB: 14;  Length: 235;
Best Local Similarity 97.0%; Pred. No. 6.2e-90;
Matches 225;  Conservative 3;  Mismatches 4;  Indels 0;  Gaps 0;

Qy   1 EPKSCDKHTCPPCPAPELLGGPSVLFPPPKPKDTIMISRTPEVTYVVDVSHEDEPEYKF 60
    4 EPKSCDKHTCPPCPAPELLGGPSVLFPPPKPKDTIMISRTPEVTYVVDVSHEDEPEYKF 63
Db   61 NWYDGVVEHNVTKTPREEQYNSTYRVSVLTVLHQWNANGKEYKCKVSNKALPAPIEKT 120
    64 NWYDGVVEHNVTKTPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 123
Db   121 ISXKVKQREPQVTLPSSRDELTKNQVSITCLVKGFPSPDIAVWESNGOPENNYKTP 180
    124 ISXKVKQREPQVTLPSSRDELTKNQVSITCLVKGFPSPDIAVWESNGOPENNYKTP 183

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181 PVLDVGSSFLYSLKLTVDSRWNQGNVFSCSVMHEALHNHYQRSLSLSPGK 232
 184 PVLDSDGSFLYSLKLTVDSRWNQGNVFSCSVMHEALHNHYTOKSLSLSPGK 235

3-SUIT 12
 Sequence 12, Application US/09996357
 GENERAL INFORMATION:
 APPLICANT: Geffter, Malcolm L

APPLICANT: Joyal, John L

APPLICANT: Gosselin, Michael

TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR

FILE REFERENCE: PPI-105

CURRENT FILING DATE: 2001-11-27

PRIOR APPLICATION NUMBER: 60/253,302

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/250,198

PRIOR FILING DATE: 2000-11-29

PRIOR APPLICATION NUMBER: 60/257,186

PRIOR FILING DATE: 2000-12-20

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 13

LENGTH: 247

TYPE: PRT

ORGANISM: Homo sapiens

3-09-996-357-13

Query Match 97.2%; Score 1225; DB 9; Length 247;

Best Local Similarity 97.0%; Pred. No. 6.6e-90;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 EPKSCDKTHTCPCPAPELGGPSVLFPPKPKDTLMISRPEVTCLVGFPSDIAVEWSNGOPENNYKTP 60

16 EPKSCDKTHTCPCPAPELGGPSVLFPPKPKDTLMISRPEVTCLVGFPSDIAVEWSNGOPENNYKTP 75

61 NWYDGVEVHNWTKPREFQYNSTYRVSVLTIVLHQNWNGKEYKCKVSNKALPAPIKT 120

76 NWYDGVEVHNWTKPREFQYNSTYRVSVLTIVLHQWLNGEKEYKCKVSNKALPAPIKT 135

121 ISZAKVQPREPOVYTLPSRDELTKNQVSLTCLVGFPSDIAVEWSNGOPENNYKTP 180

136 ISZAKGQPREPOVYTLPPERDELTKNQVSLTCLVGFPSDIAVEWSNGOPENNYKTP 195

181 PVLDVGSSFLYSLKLTVDSRWNQGNVFSCSVMHEALHNHYQRSLSLSPGK 232

196 PVLDSDGSFLYSLKLTVDSRWNQGNVFSCSVMHEALHNHYTOKSLSLSPGK 247

3-SUIT 13
 Sequence 13, Application US/10008063
 GENERAL INFORMATION:
 APPLICANT: Gross, Jane A.

APPLICANT: Henne, Randal M.

APPLICANT: Grant, Francis, J.

TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor

FILE REFERENCE: 00-103

CURRENT APPLICATION NUMBER: US/10/008,063

CURRENT FILING DATE: 2001-11-05

NUMBER OF SEQ ID NOS: 46

SOFTWARE: PastSEQ for Windows Version 4.0

LENGTH: 251

TYPE: PRT

ORGANISM: Homo sapiens

3-09-996-357-13

Sequence 13, Application US/10008063

GENERAL INFORMATION:
 APPLICANT: Geffter, Malcolm L

APPLICANT: Ireal, David I

APPLICANT: Joyal, John L

APPLICANT: Gross, Jane A.

APPLICANT: Henne, Randal M.

APPLICANT: Grant, Francis, J.

TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor

FILE REFERENCE: 00-103

CURRENT APPLICATION NUMBER: US/10/008,063

CURRENT FILING DATE: 2001-11-05

NUMBER OF SEQ ID NOS: 46

SOFTWARE: PastSEQ for Windows Version 4.0

LENGTH: 251

TYPE: PRT

ORGANISM: Homo sapiens

US-10-008-063-18

Query Match 97.2%; Score 1225; DB 14; Length 251;

Best Local Similarity 97.0%; Pred. No. 6.7e-90;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 EPKSCDKTHTCPCPAPELGGPSVLFPPKPKDTLMISRPEVTCLVGFPSDIAVEWSNGOPENNYKTP 60

20 EPKSCDKTHTCPCPAPELGGPSVLFPPKPKDTLMISRPEVTCLVGFPSDPEVKP 79

61 NWYDGVEVHNWTKPREFQYNSTYRVSVLTIVLHQNWNGKEYKCKVSNKALPAPIKT 120

80 NWYDGVEVHNWTKPREFQYNSTYRVSVLTIVLHQWLNGEKEYKCKVSNKALPAPIKT 135

121 ISZAKVQPREPOVYTLPSRDELTKNQVSLTCLVGFPSDIAVEWSNGOPENNYKTP 180

140 ISZAKGQPREPOVYTLPSRDELTKNQVSLTCLVGFPSDIAVEWSNGOPENNYKTP 195

181 PVLDVGSSFLYSLKLTVDSRWNQGNVFSCSVMHEALHNHYQRSLSLSPGK 232

200 PVLDSDGSFFLISKLTVDSRWNQGNVFSCSVMHEALHNHYTOKSLSLSPGK 251

RESULT 15

US-09-996-357-12

Sequence 12, Application US/10152363A

GENERAL INFORMATION:

APPLICANT: Rixon, Mark W.

APPLICANT: Gross, Jane A.

APPLICANT: File Reference: 01-20

CURRENT APPLICATION NUMBER: US/10/152,363A

CURRENT FILING DATE: 2002-05-20

PRIOR APPLICATION NUMBER: 60/293,343

PRIOR FILING DATE: 2001-05-24

SEQUENCE ID NOS: 70

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 6

LENGTH: 251

TYPE: PRT

ORGANISM: Homo Sapiens

US-10-152-363A-6

Query Match 97.2%; Score 1225; DB 14; Length 251;

Best Local Similarity 97.0%; Pred. No. 6.7e-90;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 EPKSCDKTHTCPCPAPELGGPSVLFPPKPKDTLMISRPEVTCLVGFPSDIAVEWSNGOPENNYKTP 60

20 EPKSCDKTHTCPCPAPELGGPSVLFPPKPKDTLMISRPEVTCLVGFPSDPEVKP 79

61 NWYDGVEVHNWTKPREFQYNSTYRVSVLTIVLHQNWNGKEYKCKVSNKALPAPIKT 120

80 NWYDGVEVHNWTKPREFQYNSTYRVSVLTIVLHQWLNGEKEYKCKVSNKALPAPIKT 135

121 ISZAKVQPREPOVYTLPSRDELTKNQVSLTCLVGFPSDIAVEWSNGOPENNYKTP 180

140 ISZAKGQPREPOVYTLPSRDELTKNQVSLTCLVGFPSDIAVEWSNGOPENNYKTP 195

181 PVLDVGSSFLYSLKLTVDSRWNQGNVFSCSVMHEALHNHYQRSLSLSPGK 232

200 PVLDSDGSFFLISKLTVDSRWNQGNVFSCSVMHEALHNHYTOKSLSLSPGK 251

RESULT 15

US-09-996-357-12

Sequence 12, Application US/10152363A

GENERAL INFORMATION:

APPLICANT: Geffter, Malcolm L

APPLICANT: Ireal, David I

APPLICANT: Joyal, John L

APPLICANT: Gross, Jane A.

APPLICANT: Henne, Randal M.

APPLICANT: Grant, Francis, J.

TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor

FILE REFERENCE: 00-103

CURRENT APPLICATION NUMBER: US/10/008,063

CURRENT FILING DATE: 2001-11-05

NUMBER OF SEQ ID NOS: 46

SOFTWARE: PastSEQ for Windows Version 4.0

LENGTH: 251

TYPE: PRT

ORGANISM: Homo sapiens

US-10-008-063-18

Query Match 97.2%; Score 1225; DB 14; Length 251;

Best Local Similarity 97.0%; Pred. No. 6.7e-90;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 EPKSCDKTHTCPCPAPELGGPSVLFPPKPKDTLMISRPEVTCLVGFPSDIAVEWSNGOPENNYKTP 60

20 EPKSCDKTHTCPCPAPELGGPSVLFPPKPKDTLMISRPEVTCLVGFPSDPEVKP 79

61 NWYDGVEVHNWTKPREFQYNSTYRVSVLTIVLHQNWNGKEYKCKVSNKALPAPIKT 120

80 NWYDGVEVHNWTKPREFQYNSTYRVSVLTIVLHQWLNGEKEYKCKVSNKALPAPIKT 135

121 ISZAKVQPREPOVYTLPSRDELTKNQVSLTCLVGFPSDIAVEWSNGOPENNYKTP 180

140 ISZAKGQPREPOVYTLPSRDELTKNQVSLTCLVGFPSDIAVEWSNGOPENNYKTP 195

181 PVLDVGSSFLYSLKLTVDSRWNQGNVFSCSVMHEALHNHYQRSLSLSPGK 232

200 PVLDSDGSFFLISKLTVDSRWNQGNVFSCSVMHEALHNHYTOKSLSLSPGK 251

US-10-008-063-18

Query Match 97.2%; Score 1225; DB 14; Length 251;

Best Local Similarity 97.0%; Pred. No. 6.7e-90;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 EPKSCDKTHTCPCPAPELGGPSVLFPPKPKDTLMISRPEVTCLVGFPSDIAVEWSNGOPENNYKTP 60

20 EPKSCDKTHTCPCPAPELGGPSVLFPPKPKDTLMISRPEVTCLVGFPSDPEVKP 79

61 NWYDGVEVHNWTKPREFQYNSTYRVSVLTIVLHQNWNGKEYKCKVSNKALPAPIKT 120

80 NWYDGVEVHNWTKPREFQYNSTYRVSVLTIVLHQWLNGEKEYKCKVSNKALPAPIKT 135

121 ISZAKVQPREPOVYTLPSRDELTKNQVSLTCLVGFPSDIAVEWSNGOPENNYKTP 180

140 ISZAKGQPREPOVYTLPSRDELTKNQVSLTCLVGFPSDIAVEWSNGOPENNYKTP 195

181 PVLDVGSSFLYSLKLTVDSRWNQGNVFSCSVMHEALHNHYQRSLSLSPGK 232

200 PVLDSDGSFFLISKLTVDSRWNQGNVFSCSVMHEALHNHYTOKSLSLSPGK 251

RESULT 15

US-09-996-357-12

Sequence 12, Application US/10152363A

GENERAL INFORMATION:

APPLICANT: Geffter, Malcolm L

APPLICANT: Ireal, David I

APPLICANT: Joyal, John L

APPLICANT: Gross, Jane A.

APPLICANT: Henne, Randal M.

APPLICANT: Grant, Francis, J.

TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor

FILE REFERENCE: 00-103

CURRENT APPLICATION NUMBER: US/10/008,063

CURRENT FILING DATE: 2001-11-05

NUMBER OF SEQ ID NOS: 46

SOFTWARE: PastSEQ for Windows Version 4.0

LENGTH: 251

TYPE: PRT

ORGANISM: Homo sapiens

US-10-008-063-18

Query Match 97.2%; Score 1225; DB 14; Length 251;

Best Local Similarity 97.0%; Pred. No. 6.7e-90;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 EPKSCDKTHTCPCPAPELGGPSVLFPPKPKDTLMISRPEVTCLVGFPSDIAVEWSNGOPENNYKTP 60

20 EPKSCDKTHTCPCPAPELGGPSVLFPPKPKDTLMISRPEVTCLVGFPSDPEVKP 79

61 NWYDGVEVHNWTKPREFQYNSTYRVSVLTIVLHQNWNGKEYKCKVSNKALPAPIKT 120

80 NWYDGVEVHNWTKPREFQYNSTYRVSVLTIVLHQWLNGEKEYKCKVSNKALPAPIKT 135

121 ISZAKVQPREPOVYTLPSRDELTKNQVSLTCLVGFPSDIAVEWSNGOPENNYKTP 180

140 ISZAKGQPREPOVYTLPSRDELTKNQVSLTCLVGFPSDIAVEWSNGOPENNYKTP 195

181 PVLDVGSSFLYSLKLTVDSRWNQGNVFSCSVMHEALHNHYQRSLSLSPGK 232

200 PVLDSDGSFFLISKLTVDSRWNQGNVFSCSVMHEALHNHYTOKSLSLSPGK 251

RESULT 15

US-09-996-357-12

Sequence 12, Application US/10152363A

GENERAL INFORMATION:

APPLICANT: Geffter, Malcolm L

APPLICANT: Ireal, David I

APPLICANT: Joyal, John L

APPLICANT: Gross, Jane A.

APPLICANT: Henne, Randal M.

APPLICANT: Grant, Francis, J.

TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor

FILE REFERENCE: 00-103

CURRENT APPLICATION NUMBER: US/10/008,063

CURRENT FILING DATE: 2001-11-05

NUMBER OF SEQ ID NOS: 46

SOFTWARE: PastSEQ for Windows Version 4.0

LENGTH: 251

TYPE: PRT

ORGANISM: Homo sapiens

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; APPLICANT: Gosselin, Michael
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR
; CURRENT FILING DATE: 2001-11-27
; PRIORITY NUMBER: US/09/996,357
; PRIORITY NUMBER: 60/253,302
; PRIOR FILING DATE: 2000-11-17
; PRIORITY NUMBER: 60/250,198
; PRIOR FILING DATE: 2000-11-29
; PRIORITY NUMBER: 60/257,186
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 12
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence:alpha-beta(16-30)FC
; US-09-996-357-12

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	Query Match	Score	DB	Length
Qy	Best Local Similarity	97.2%	9	267;
Db	Matches	97.0%	Pred. No.	7.2e-90;
Qy	Conservative	3	Mismatches	4;
Db	Indels	0	Gaps	0;
Qy	1	EPKSCDKTHTCPPCPAPELGGPSVLFPPPKPDTLMISRTPEVTCVVVDVSHEDPVVKF	60	
Db	36	EPKSCDKTHTCPPCPAPELGGPSVLFPPPKPDTLMISRTPEVTCVVVDVSHEDPVVKF	95	
Qy	61	NWYVDGEVHNVRKTRKEEQNSTRVSVLTVLHQNWNGREKCKVSNKALPAPBKT	120	
Db	96	NWYVDGEVHNVRKTRKEEQNSTRVSVLTVLHQDWLNGREKCKVSNKALPAPBKT	155	
Qy	121	ISKAKVPREPOVYTLPPSRDELTKNQSVLCLYRGFYPSDIAVENEENGOPENNNYKTP	180	
Db	156	ISKAKGPREPOVYTLPPSRDELTKNQSVLCLYRGFYPSDIAVENEENGOPENNNYKTP	215	
Qy	181	PVLDVGSGFLYSLKLTVDSRQWQGNGFSCSVMEHALHNYQORSLSSPGK	232	
Db	216	PVLDVGSGFLYSLKLTVDSRQWQGNGFSCSVMEHALHNYTQSLSSPGK	267	

Search completed: October 27, 2004, 17:20:19
Job time : 72.0036 secs